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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                    AX167589
BC014825
RATCAMPKAA
                                                                                                                                      SUMMARIES
                                                                                                                                                                         HS272L161
AX399682
BC032787
AF428261
AK095713
BC021840
AF428262
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D86556
AF181984
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AX166520
AB021864
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CBRG46J06
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BC017634
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AX167587
AX167585
AF286366
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                                                 March 15, 2003, 05:00:47; Search time 4276 Seconds
    GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                 nucleic search, using frame_plus_p2n model
                                                                                                                                                         2054640 seqs, 14551402878 residues
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Listing first 45 summaries
                                                                                                          BLOSUM62
Xgapop 10.0 , Ygapext (
Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                     Database :
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AL049688 Human gen AX399682 Sequence BC032787 Homo sapi AK095713 Homo sapi BC021840 Mus muscu BC051840 Mus muscu DE6557 Rattus norv AX16557 Sequence AX16557 Sequence AX167585 Sequence AX167585 Sequence AX167589 Sequence BC014825 Mus muscu L26288 Rattus norv L41816 Homo sapien L26288 Rattus norv AR181984 Mus muscu AX16520 Sequence BC014825 Mus muscu AX16520 Sequence AB0427 Rattus norv AR181984 Mus muscu AX16520 Sequence AB023027 Mus muscu AX16520 Sequence AR03184 ACC Rattus norv AR19194 Mus muscu AX16520 Sequence

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AL365314 Mouse DNA AC022675 Mus muscu M64176 D.discoideu

Rattus norv

Ca2+/calmod Rat Ca++/ca

X58995 Mouse mRNA S65840 Ca2+/calmod M64757 Rat Ca++/ca

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Best Local Similarity:
Query Match:
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 432
                                          Scores:
BASE COUNT
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CGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKA
             HS272L161 1738 bp mRNA linear PRI 21-APR-1999 Human gene isolated from PAC 272L16, chromosome 1, similar to calcium/calmodulin dependent protein kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAAAVVHHMRKLHMNLHSPGV
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                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1738)
                                                                                                                                                                               Submitted (21-APR-1999) E-mail contact: humquery@sanger.ac.uk Submitted (21-APR-1999) E-mail contact: humquery@sanger.ac.uk Striks sequence was generated from cDNA clones isolated using sequence from the bacterial clone 272L16 (AL023754) and EST data. The EST sequences listed match this sequence with an identity of least 95% between the coordinates shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="matches EST AI215131 from clone IMAGE:1925595"
                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/HGP/Chr1/ Partial, experimentally
determined gene.
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Location/Qualifiers
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0
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                                      Conservative:
Mismatches:
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Matches:
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357
                                                                      US-09-960-643-2 (1-476) x HS272L161 (1-1738)
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                         2.33e-170
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	Percent Similarity: 100 Best Local Similarity: 100 Query Match: 100 DB: 6	-096-60-	OY I MECGLYANGLYSCIUG. 1 1 1 1 1 1 1 1 1 1	-	Oy 41 LysGlnArgLeuThrG 	Qy 61 ArgAspSerSerLeuG	Db 250 CGGGACAGCAGCTGG Qy 81 ValThrLeuGluAspI	310	OY 101 SerG1761V61V6ULEUP. 	121	430	Oy 141 HisargaspLeuLysP	161	550	Qy 181 GlyThrProGlyTyrV	Db 610 GGGACCCCAGGCTACG		670		241	Db 790 CCATTCTGGGATGACA	261	850	Db 910 ACGCCCTCCACCGG	Qy 301 LysSerLysTrpArgG
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Qy 301 Db 918	Qy 321 Db 978	Oy 341	Oy 361		Db 1158 Qy 401	Db 1218	Qy 421 Db 1278		DD 1338 Qy 461	Db 1398	RESULT 2 AX399682	LOCUS DEFINITION ACCESSION	VERSION KEYWORDS	SOURCE ORGANISM	000000000000000000000000000000000000000	AUTHORS	JOURNAL	FEATURES SOURCE	CDS						BASE COUNT ORIGIN

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2447
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Contact: MGC help desk
Email: cgapbs.rfmail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@hngri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maskello,C., Maskeri,B., Mastiian,S.D.,Mccloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC032787 27-JUN-2002 Homo sapiens, calcium/calmodulin-dependent protein kinase IG, clone MGC:44894 IMAGE:5179957, mRNA, complete cds.
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg, R.
Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                         1330 AGCTGCCTGAACATTGGGAGCAAAGGAAAGTCCTCCTACTGCTCTGAGCCCACACTCCTC 1389
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                                                                                                                                                               LeuAspHisSerValAlaLeuProAlaLeuThrGlnLeuProCysGlnHisGlyArgArg 380
                                                                                                                                                                                                                                                                                                                            420
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  HisMetAsnLeuHisSerProGlyValArgProGluValGluAsnArgProProGluThr
                                                                                GlnAlaSerGluThrSerArgProSerSerProGluIleThrIleThrGluAlaProVal
                                                                                                                                                                                                                                                                                                                            SerSerLeuValProMetHisGlnGlySerLeuAlaAlaGlyProCysGlyCysCysSer
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Mammalia; Eutheria; Primates;
1 (bases 1 to 2474)
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Clone distribution: MGC clone distribution information can be found

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/product="calcium/calmodulin-dependent protein kinase IG"
/product="calcium/calmodulin-dependent protein kinase IG"
/product="calcium/calmodulin-dependent protein kinase IG"
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/d
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 68 Row: k Column: 17
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gl: 14196444.
Location/Qualifiers
                                                                                                                                                                                                              /organism="Homo sapiens"
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gamma

EMRB,

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- GARGE - CAMKIG"
- GARGE - CAMKIG"
- GARGE - CAMKIG"
- GARGE - CAMKIGNG - 
Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases I to 2464)

Schutte, B.C., Bjork, B.C., Coppage, K.B., Malik, M.I., Gregory, S.G.,

Scott, D.J., Brentzell, L.M., Matanabe, Y., Dixon, M.J. and Murray, J.C.

A preliminary gene map for the Van der Woude syndrome critical
region derived from 900 kb of genomic sequence at 1q32-q41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product = "calcium/calmodulin-dependent protein kinase
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2 (bases 1 to 2464)

Bjork, B.C., Watanabe, Y., Murray, J.C. and Schutte, B.C.
Characterization of the human ortholog of rat CaM Kinase
(CamKIG) at 1q32-q41
                                                                                                                                                                                                                                                                                                         Genetics, University of Iowa,
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Blork, BC., Watanabe, Y., Murray, J.C. and :
Direct Submission
Submitted (05-0CT-2001) Genetics, Universion
Iowa City, IA 52242, USA
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
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73. .1503
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AUTHORS
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                                                                                 LeuAspHisSerValAlaLeuProAlaLeuThrGlnLeuProCysGlnHisGlyArgArg
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                                                              GlyThrProGlyTyrValAlaProGluValLeuAlaGlnLysProTyrSerLysAlaVal
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Db 1333 AGCIGCCTGAACATIGG	1393	Qy 461 GlySerSerHisCysArc 	RESULT 5 AK095713 LOCUS AK095713 DEFINITION Homo, sapiens CDM	ION N DS	SOURCE HOMO SADIENS IER CLONE:FEBRA2007; ORGANISM HOMO SADIENS EUKARYOLA: MELAS	Manuhalia; buller REFERENCE 1 AUTHORS Tanigami,A., Fu Shimizu,F., Wake	SUGIYAMA;I., II. Yamanoto,J., Isr Yamaza,K., Yamas Kimura,K., Yamas	TITLE NEDO human CDNA JORGNAL Unpublished	KEFERCE 2 (DASES I LO. AUTHORS ISOQAI, T and YE TITLE Direct Submissic JOURNAL Submitted (04-07)	KAZUSE NAMENITALIS COMMENT NEDO human CDNA ECONOMY, Trade &	research Associated to the construction: Wey Technology (EVALUATION; CION RAB; annotation FEATURES Location Source 1. 265	/organ /db_xrc /clonex	OUNT 619 a	ent Scores: No.:	Scont Similarity: 99.79 Best Local Similarity: 99.79 Query Match:	-09-960-643-2 (1-476)	Oy 1 MetGlyArgLysGluGlı
11111111111111111111111111111111111111	/ 81 ValThrLeuGluAspileTyrGluSerThrThrHiSTyrTyrLeuValMetGlnLeuVal 100 	101 SerGlyGlyGlyGluLeuPheAspArgIleLeuGluArgGlyValTyrThrGluLysAspAla 120 	121 SerLeuvalIleGinGinValLeuSeralaValLySTyrLeuHisGluAsnGlyIleVal 140 	141 HisargaspLeuLysProGluAsnLeuLeuTyrLeuThrProGluGluAsnSerLysIle 160 	161 MetileThrAspPhedlyLeuSerLysMetGluGlnAsnGlylleMetSerThrAlaCys 180	/ 181 GlyThrProGlyTyrValAlaProGluValLeuAlaGlnLysProTyrSerLysAlaVal 200	201 AspCysTrpSerIleGlyValIleThrTyrIleLeuLeuCysGlyTyrProProPheTyr 220 	<pre>221 GluGluThrGluSerLysLeuPheGluLysIleLysGluGlyTyrTyrGluPheGluSer 240 111111111111111111111111111111111111</pre>	y 241 ProPheTrpAspAspIleSerGluSerAlaLysAspPheIleCysHisLeuLeuGluLys 260	/ 261 AspproAsnGluargTyrThrCysGluLysAlaLeuSerHisProTrpIleAspGlyAsn 280 	281 ThralaLeuHisargAspIleTyrProSerValSerLeuGlnIleGlnLysAsnPheAla 300	901 LysSerLysTrpargGlnAlaPheAsnalaAlaValValHisHisMetArgLysLeu 320 	321 HismetasnLeuHisSerProGlyValargProGluValGluAsnArgProProGluThr 340	341 GinalaserGluthrSerargProSerSerProGluIleThrIleThrGlualaProVal 360 	361 LeuAspHisSerValAlaLeuProAlaLeuThrGlnLeuProCysGlnHisGlyArgArg 380 	381 ProfhralaProGlyGlyArgSerLeuAsnCysLeuValAsnGlySerLeuHislleSer 400 	/ 401 SerSerLeuValProMetHisGlnGlySerLeuAlaAlaGlyProCysGlyCysCysSer 420 	/ 421 SerCysLeuAsnIleGlySerLysGlyLysSerSerTyrCysSerGluProThrLeuLeu 440
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(14-UTL-2002) Takao Isogal, FLJ Project(HRI Team); 2-6-7

(tarl, Kisarazu, Chiba 292-0812, Japan

(tarl, Kisarazu, Chiba 292-0812, Japan

(omicséhri.co.)p, Tel:81-81-839-52-3975, Fax:81-438-52-3986)

CDNA sequencing project supported by Ministry of

ade and industry of Japan, CDNA full Insert sequencing:

ade and industry of Japan, CDNA full Insert sequencing:

n: Helix Research Institute (HRI) (supported by Japan

ogy Center etc.); 5'- & 3'-end one pass sequencing: RAB,

ottechnology Center, National Institute of Technology and

clone selection for full insert sequencing: HRI and

tion: HRI and RAB.
                                                                                                                                                                                                                           2612 bp mRNA linear PRI 15-JUL-2002
DNA FLJ38394 fis, clone FEBRA2007534, moderately
KI-like protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ujiwara,T., Shibahara,T., Goto,Y., Hirao,M.,
kebe,H., Ono,T., Hishigaki,H., Watanabe,T., Ozaki,K.,
ribe,R., Otsuki,T., Saro,H., Wakamatav,A., Ishii,S.,
ribe,R., Mawai-Hio,Y., Saito,K., Nishikawa,T.,
sshita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
nda,K., Wagatsuma,M., Murakawa,K., Kanehori,K.,
i,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
i,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
A sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                         azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Primates; Catarrhini; Hominidae; Homo.
fis (full insert sequence).
etal brain cDNA to mRNA, clone_lib:FEBRA2
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e_lib="FBBRA2"
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ref="taxon:9606"
e="FEBRA2007534"
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		ULEUTYTEUTHTPTCGIUGIUASNSETLYSIIe 16	######################################		ValargproGluValGluAsnargProProGluThr 340
LysThrPhellePhemetGluva.	ValThrLeuGluAspIleTyrG 		AspCysTrpSerIleGlyVallle	AspProAsnGluArg	HismetasnLeuHisSerProG
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67 67 67 68 69 64		Oy Oy Oy	07 07 08 09 09	OY OY OY OY	0

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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
Tissue Proturement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web Site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Gunrartne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 41 Row: i Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROD 07-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 2416)
Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus, clone MGC:30513 IMAGE:4502479, mRNA, complete cds. BC021840.1 GI:18256866 MGC.
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Submitted (18-ZAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
1505
                                                                                                                                                                                                                                                                            1566 AAAAAGGCCAACAAAAAAACTTCAAGTCGGAGGTCATGGTACCAGTTAAAGCCAGT 1625
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                                                                               421 SerCysLeuAsnIleGlySerLysGlyLysSerSerTyrCysSerGluProThrLeuLeu
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/protein_id="AAH21840.1"
/db_xref="GI:18256867"
                                                                                                                                                                                                                                                                                                                                   1. .2416
//Organism="Mus musculus"
/db_xref="taxon:10090"
/clone="MGC:30513 IMAGE:4502479"
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/translation="MGRKEEEDCSSWKKQTINIRKTFIFMEVLGSGAFSEVFLVKQRV
TGKLFALKCIKKSPAFRDSSIDENEIATHLARKHEINTVILEDITSETTHYILMQLVSG
GELFORILEGGYYTERCASLVIQVLSAVKYLHENGIYHRDLKPENLLYILPEENSKI
MITDFGLSKMEQNGVWSTACGTPGYVAPEVLACKPYSKAVDCWSIGVITYILLCGYPP
TSTETESKLFERKIRGYYEPESPFWDDISESARDFIGHLLERDPDRERYTCERALRHPW
IDGRITALHRDIYPSYSLQIQRNFALSKWRQAFNAAAVVHHRKKLHMNLHSFSYRQEVE
NRPPVSPAPEVSRPDSHDSSITEAFILDPSTPLPALTRLPCSHSSRPSAPSGGRSLNC
KINGSLRISSSLVPMQQGPLATGPCGCCSSCLNIGNKGKSSYCSEPTLFRKANKKQNF
KSPWYPVKAGGTYCVLWM"

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Matches:
Conservative:
Mismatches:
Indels:
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94.97%
92.03%
92.62%
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cal Similarity:
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DB:
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       LysSerLysTrpArgGlnAlaPheAsnAlaAlaAlaValValHisHisMetArgLysLeu
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu

Bukaryota; Metazoa; Chordata; Ciurognathi; Muridae; M

1 (bases 1 to 2427)

1 (bases 1 to 2427)

1 (bases 2 to 2427)

1 (bases 3 to 2427)

1 (bases 3 to 2427)

1 (bases 4 to 2427)

2 (bases 1 to 2427)

3 (bases 1 to 2427)

5 (bases 1 to 2427)

6 birect Submission
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Sciurognathi; Muridae;
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AF428262.1 GI:16755793
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Iowa City, IA 52242, USA

Location/Qualifiers

e 1. .2427

/organism="Mus musculus"

/db_xref="taxon:10090"

/chromosome="1" /map="1H, 104.00 cM"
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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AUTHORS
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Sciurognathi; Muridae; Murinae;
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Yokokura, H., Terada, O., Naito, Y. and Hidaka, H.
Isolation and comparison of rat cDNAs encoding
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or Protein Kinase,
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Rattus norvegicus
Eukaryota; Metazoa; Chordata;
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D86557
D86557.1 GI:2077933
Protein kinase.
Rattus norvegicus embryo
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MITDFGLSKMEQNGVMSTACGTPGYVAPEVLAOKPYSKAVDCWSIGVITYILLCGYPP
FYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALRHPW
                                                                                                                                                                                       IDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAAAVVHHMRKLHMNLHSPSVRQEVE
NRPPVSPAPEVSRPDSHDSSITEAPILDPSTPLPALTRLPCSHSSRPSAPSGGRSLNC
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Matches:
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Mismatches:
Indels:
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694 c 601 g 547 t
                      /note="corresponds to EST
                                                                                                           /protein_id="AAL28101.1"
                                                                                                                                                                                                                                                                                                                                      Gaps:
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/clone="IMAGE:4502479"
           /tissue_type="retina'
                                                                /gene="Camklg"
                                          /gene="Camklg"
                                                                             /codon_start=1
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2327.50
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 107).
Plowman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R., Flanagan, P. and Clary, D.S.
Novel human protein kinases and protein kinase-like enzymes Patent: WO 0138503-A 8 31-MAY-2001;
Sugen, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                              ProPheTrpAspAspIleSerGluSerAlaLysAspPheIleCysHisLeuLeuGluLys
                                                                                                                                                                                                                                                                                                                                                        AspProAsnGluArgTyrThrCysGluLysAlaLeuSerHisProTrpIleAspGlyAsn
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Vokokura, H.
Direct Submission
Submitted (15-7UL-1996) Hisayuki Yokokura, Nagoya University School
of Medicine, Department of Pharmacology; Tsurumai 65, Showa-ku,
Nagoya, Aichi 466, Japan (Tel:052-744-2075, Fax:052-744-2083)
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/clone="85"
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Donoho, G., Scoville, J., Turner, C.A., Friedrich, G., Zambrowicz, B. Abuin, A. and Sands, A.T.
Novel human kinase proteins and polynucleotides encoding the sam Nevel human kinase proteins and polynucleotides encoding the sam Lexicon Genetics Incorporated (US)
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Donoho, G., Scoville, J., Turner, C.A., Friedrich, G., Zambrowicz, B., Abuin, A. and Sands, A.T.
Novel human kinase proteins and polynucleotides encoding the same Patent: WO 0142435-A 114-JUN-2001; Lexicon Genetics Incorporated (US)
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/db_xref="taxon:9606"
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Homo sapiens CamKI-like protein kinase mRNA, complete cds.
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Submitted (11-JUL-2000) Dept. Pulmonary Diseases, University
Medical Center Utrecht, Heidelberglaan 100, Utrecht 3584 CX,
                                                                                                          GlyAsnThrAlaLeuHisArgAspIleTyrProSerValSerLeuGlnIleGlnLysAsn
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ValSerGlyGlyGlyLeuPheAspArgIleLeuGlyArgGlyValTyrThrGlyLysAsp
                                                      AlaSerLeuValIleGlnGlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIle
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Butele
Bukarmalia: Butheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 1579)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Verylogen, S., Koenderman, L. and Coffer, P.J.
Identification and characterization of CKLiK: a 1Ca2+/Calmodulin-dependent kinase
Blood (2000) In press
2 (bases 1 to 1579)
Verploegen, S. and Coffer, P.J.
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Enkaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1671)

Donoho, G., Scoville, J., Turner, C.A., Friedrich, G., Zambrowicz, B., Abuin, A. and Sands, A.T.

Abuin, A. and Sands, A.T.

Novel human kinase proteins and polynucleotides encoding the same betent: WO 0142435-A 5 14-JUN-2001;

Loation Genetics Incorporated (US)
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                  GluLysAspProAsnGluArgTyrThrCysGluLysAlaLeuSerHisProTrpIleAsp
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/organism="Homo sapiens"
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Sequence 5 from Patent W00142435.
AX167589 GI:14596988
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ξ q	100	ValSerGlyGlyGluLeuPheAspArglleLeuGluArgGlyValTyrThrGluLygAsp 119 	
ξ, q	120	AlaserLeuvallleGlnGlnValLeuserAlavalLysTyrLeuHisGluAsnGlylle 139 ::: ::	
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્ર વ	160	IleMetileThraspPheGlyLeuSerLysMetGluGlnasnGlyIleMetSerThr 178 	
λ q	179	AlacysGlyThrProGlyTyrValAlaProGluValLeuAlaGlnLysProTyrSerLys 198 	
Zg qg	199	AlaValAspCysTrpSerIleGlyValIleThrTyrIleLeuLeuCysGlyTyrProPro 218 	
<u>ک</u> ۾	219	ysGluGlyTyrTyrGluPhe 2 ::: TCAAGGGGAATATGAGTTT 8	
<u>ک</u> و	239	GluserProPheTrpaspaspleserGluseralaLysaspPheIleCysHisLeuLeu 258 	
<u>ک</u> و	259	GluLysaspProdsnGluArgTyrThrCysGluLysalaLeuSerHisProfrpIleasp 278 	
Z q	279		
∑. q	299	ഗര	
દ્ર વ	319		
<u>ک</u> و	337	ProGluThrGlnAlaSerGluThrSerArgProSerSerProGluIleThrIle 355 ::::: ::::: ::::: AGCCAAAAAGACTGTGGGTATGTAGGAAAACCAGAAATC-CCTCAGCTGACAGTG 124	
≿ 4		rGluAlaProValLeuAspHisSerValAlaLeuProAla	
. >	37	LeuThrGlnLeuProCvs	
. <u>გ</u>	1305	 GGGCTTTCTATACTTAATCCCATGTCATGCGACCCTAGGACTTTTTTAACATGTAAT 13	
<u>~</u> 4	37(379	
2 2	380	CACGCCIGIAAICCCAACACIT	
, <u>A</u>	0 0	AGGACTGTTTGAGTTCAGGAGTTTTAAGACCAGCTGACCAACATGGTGAAACCCCATC 14	

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAK Plate: 23 ROW: j Column: 19 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

Location/Qualifiers

1. .1448

// Clone "MGC: 18933 IMAGE: 3963343"

// Clone "MGC: 18933 IMAGE: 3963343"

// Clone "MGC: 18933 IMAGE: 3963343"

// Clone "MGC: 10 month old virgin mouse. Taken by blopsy."

// Clone lib "NGI CGAP_MAMM"

// Clone lib "NGI CGAP_MAMM"

// Clone lib "NGI CGAP_MAMM"

// Clone lib "NGI CGAP_MAMM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing Dy: Baylor College of Medicine Human Genome
Sequencing Center
CGHET COGE: BCM-HGSC
Web Site: http://www.hgsc.bcm.tmc.edu/cdna/
COntact: amg@bcm.tnc.edu
Gunnarhen, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
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kinase I"
/kinase I"
/kinase I"
/db_xref="GI:15928726"
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Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 1448)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammallan
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                               1485 TCTACTAAAATATAAAAATTAGCCGGGTGTGGTGGCGGACCACTGTAATGTCAGCTACTT 1544
                                                                                                           395 GlySerLeuHisIleSerSerSerLeuValProMetHisGlnGlySerLeuAlaAlaGly 414
                                                                                                                                                                                                                     415 ProCysGlyCysCysSerSerCysLeuAsnIleGlySerLysGlyLysSerSerTyrCys 434
-----GlyGlyArgSerLeuAsnCysLeuValAsn 394
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Mus musculus, Similar to calcium/calmodulin-dependent protein kinase 1, clone MGC:18933 IMAGE:3969343, mRNA, complete cds.
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                                                                                                                                        /note="Vector: pCMV-SPORT6"
120. .1244
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Mus musculus
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us-09-960-643-2.p2n.rge

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/translation="MpGAVEGPRWKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQK
LVAIKCIRKRALEGKEGSMENBIAVLHKIRNIVALDDIYESGGHEYLIMOLVSGGE
LFDRIVEKGFYTERDASRLIFQVLDAVKYLHDLGIVHRDLKPENLLYYSLDEDSKIMI
SDFGLSKMEDPGSVLGTRGGYVAPEVLAQKPYSKAVDCWSIGYLAYILLCGYPPP
YDENDAKLFEQILKAEYEFDSPYWDDISDSAKDFIRHLMEKDPEKRFTCEQALQHPWI
AGDTALDKNIHGSVSEQIKKNRAKSKWKQAFWATAVYRHMRKLQLGTSOEGGGOTGSH
GELLIPTAGGPAGCCRDCCVPEGSELPPAPPPSSRAMD"

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Matches:
Conservative:
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Indels:
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LysAlaLeuSerHisProTrpIleAspGlyAsnThrAlaLeuHisArgAspIleTyrPro 289

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/translation="MPGAVEGPRWKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQK
LIVAIKCIAKRALEGKEGSABERTAVLHKIKHHNIYALDDIYEGGGHLYLINDLVSGGE
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AGDTALLDKINHQSVSBOIKKNRPAKSKWKQAENATAVVRHMRKLQLGTSQEGGGGTASH
GELLTPITAGGPAAGCCCRDCCVEPGSELPPAPPSSRAMD"
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                                                                                                                        1284 GAGGCAGCCTGCTTCCTCCTCACTCCAGATCTGGGGCGTTTCTGACCCCACACCTCTTCA 1343
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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SerValSerLeuGlnIleGlnLysAsnPheAlaLysSerLysTrpArgGlnAlaPheAsn
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                                                                                                                                                                                                                                 ------AsnArgProGluValGlu-----AsnArgProPro
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Cho,F.S., Phillips,K.S., Bogucki,B. and Weaver,T.E.
Characterization of a rat cDNA clone encoding
calcium/calmodulin-dependent protein kinase I
Biochim. Biophys. Acta 1224 (1), 156-160 (1994)
95035115
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/db_xref="taxon:10116"
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465	449 PheLysSerGluValMetValProyalLysAlaSerGlySerSerHisCys 465	449	Qγ
1244	4 CICAGAACIGCCCCCIGCACCACCCCCAAGCICIAGGGCCAIGGACIGAAA	1194	QQ
448	429 GlyLysSerSerTyrCysSerGluProThrLeuLeuLysLysAlaAsnLysLysGlnAsn 448	429	δy
1193	5 CCCACACAGCTGGGGGCCAGCAGCTGCTGCTG-TCGAGACTGCTGTGTGGAGCCAGG	1135	qq
428	410 SerLeuAlaAlaGlyProCysGlyCysCySerSerCysLeuAsnIleGlySerLys	410	ΟŊ
1134	1132 ACA	1132	qq
409	390 AsnCysLeuValAsnGlySerLeuHisIleSerSerSerLeuValProMetHisGlnGly 409	390	δy
1131	0	1090	qq
389	370 LeuThrGlnLeuProCysGlnHisGlyArgArgArgProThrAlaProGlyGlyArgSerLeu	370	QY
1089	6	1089	Op
369	0 SerProGluIleThrIleThrGluAlaProValLeuAspHisSerValAlaLeuProAla	350	Qy
1089	4ACCAGC	1084	qq
349	330 ArgProGluValGluAsnArgProProGluThrGlnAlaSerGluThrSerArgProSer	330	Qy
1083	1042 GCTACCGCTGTGGTTCGGCACATGAGGAAGCTGCAGCTGGGC	1042	QQ

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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March 14, 2003, 13:47:15 ; Search time 7161 Seconds
   (without alignments)
   9944.779 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			% Query					
No.	Sco	re	Match	Length	DB	at	11 11 11 11 11 11 11 11 11 11 11 11 11	Description
1		47	100.0	2447	9	AX399682		AX399682 Sequence
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ν) «		C C	98.7	2464		AF428261		AF428261 Homo sapi
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9	-	ب د	54.3	2416		BC021840		BC021840 Mus muscu
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110		٥٧	20.0	1671		AF 286366		AFZ86366 HOMO Sapı
12		2 0	20.0	1074	_	AX166517		AX166517 Sequence
13		. 7	20.5	1074		AX167587		AX167587 Sequence
14		. 2	20.5	1158	9	AX167585		AX167585 Sequence
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16		8.5	20.0	1480	σ,	HUMCKI		L41816 Homo sapien
17		S i	9.6	1402		RATPRKI		L24907 Rattus norv
18		000	7.7	1648		BC014825		BC014825 Mus muscu
25		0 <	 	1033		AB00426/		ABUU426/ Kattus no
202		7 7	17.5	1332		AB02302/ D86556		ABU2302/ Mus muscu
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25		4	11.9	1546		AB021864		AB021864 Caenorhab
26		06	11.9	3316		DME17917		Y17917 Drosophila
		φ.	11.8	182054	10	AL365314		AL365314 Mouse DNA
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33		9	10.0	1503		AX239863		AX239863 Sequence
34		9	10.0	2297		AX239861		AX239861 Sequence
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36		9.	10.0	3012		BC000497		BC000497 Homo sapi
37		9.	10.0	3012		BC005828		BC005828 Homo sapi
38		۰	10.0	3018		BC017363		BC017363 Homo sapi
χ. •		ه د	10.0	3057		BC019256		BC019256 Homo sapi
40		٥	10.0	3124		AX350342		AX350342 Sequence
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ACCESSION VERSION		AX39	AX399682 AX399682.1	GI:2	13354	155		
KEYWORDS	SC	. 4	,					
ORGANI	SM	Homo Euka	Homo sapiens Eukaryota; M	ns Metazoa		Chordata; Cran	iata; Vertebrata;	ata; Euteleostomi;
REFERENCE	Œ	Mammaîj 1	alia;	Eutheria			Catarrhini; Homin	• •
AUTHORS	ı w	Dela Cance	belaney,A.D. Cancer associ	D. and ociated	Yoga	,A.D. and Yoganathan,T. associated protein kinases	and their uses	80
JOURNAL	Į.	Patent:	nt: WO	022494	17-A	3 28-MAR-2002		R

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TEAL ALTON - "MORKEEDDCSSWKKQTTNIRKTFIFMEVIGSGAFSEVFLVKQRL
TGKLFALKCIKKSPAFRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSG
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VNGSLHFSSSLVPMHQSSLAAGPCGCCSSCLNIGSKGKSSYCSEPTLLKKANKKQNFK
SEVMYPVKASGSSHCRAGGTGVCLIM"
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/db_xref="taxon:9606"
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PBPACS SPEED YSSAMBER	TN Pa FEATURES SOUICE	CDS		BASE COUNT ORIGIN Query Match Best Local C	Matches 2446 Qy 1 TGGA Db 1 TGGA Qy 61 CTGG Db 61 CTGG	121 121 181 181	Oy 241 CCTGG Db 241 CCTGG OY 301 GAAAA OY 301 GAAAA OY 301 GAAAA OY 301 CAGC
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TEALER LION- MORREEDDCSSWKKQTTNIRKTFIFMEVIGSGAFSEVFLVKQRL
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Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haphighi,P.,
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Maduro,Q.L., Masiello,C., Maskerl,B., Mastrian,S.D., McCloskey,J.C.
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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CAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCTGGAGCGGGGTGTCTACACAGAG	AAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAATACCTACATGAGAT 	GGCATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCTTTACCTTACCCTGAAGAGACCIIIIIIIIII	TCTAAGATCATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGGCATCATGTCC 	- ACTGCCTGTGGGACCCCAGGCTACGTGGCTCCAGAAGTGCTGGCCCAGAAACCCTACAGC	AAGGCTGTGGATTGCTGGTCCATCGGCGTCATCACCTACATATTGCTCTGTGGATACCCC	CCGTTCTATGAAGAAACGGAGTCTAAGCTTTTCGAGAAGATCAAGGAGGGCTACTATGAG	TTTGAGTCTCCATTCTGGGATGACATTTCTGAGTCAGCCAAGGACTTTATTTGCCACTTG	CTTGAGAAGGATCCGAACGAGCGGTACACCTGTGAGAAGGCCTTGAGTCATCCCTGGATT	GACGGAAACACGCCCTCCACCGGACATCTACCCATCAGTCAG	AACTTTGCTAAGGGGAAGTGGAGGCAAGCCTTCAACGCAGCAGCTGTGGTGGTGCACCACATG	- AGGAAGCTACACATGAACCTGCACAGCCCGGGCGTCCCCCAGAGGTGGAGAAACAGGCCG	CCTGAAACTCAAGCCTCAGAAACCTCTAGACCCAGCTCCCCTGAGATCACCATCACCGAG	GCACCTGTCCTGGACCACAGTGTAGCACTCCCTGCCCTG	GGCCGCCGGCCCACTGCCCCTGGTGGCAGGTCCCTCAACTGCCTGGTCAATGGCTCCCTC	CACATCAGCAGG	TGCTGCTCCAGCTGCCTGAAC	ACACTCCTCAAAAAAGGCCAACAAAAAACAGTACAAGTCGGAGGTCATGGTACCAGTT	. AAAGCCAGTGGCAGCTCCCACTGCCGGCAGGCAGACTGGAGTCTGTCT
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g	Oy Db	Qy Dp	Qy	o o	o o	o S	Qy Dp	Oy Dp	Qy Dp	ço g	oy Op	S G	Oy Op	Oy Op	Oy Dp	Qy	Oy Dp	Qy Db

linear PRI 07-NOV-2001 protein kinase I gamma 2340 1920 1920 1980 1980 2040 2040 2100 2100 2160 2220 2400 2400 TGCGCTGAGACCCAGCCAGCACACTTCTGGCCCTTCTCCCTGCCTCAATCTAAAAGCAGT GGTGCCCACCAGCTTCCAGGTCTCCCTGACCTGCTCTATGCCCCACACACCTACGTG CCGTGGCTCTGTGCAGTGTACGTAGATAGCTCTCGCCTGGGTCTGTGCTGTTTGTCGTGA ATCCTGGCCACATGTCCTCCGTGCACACACCCAATGGAGTTAACCTTGGAAGTTGACTAT ATCCTGGCCACATGTCCTCCGGTGCACACACCCAATGGAGTTAAACCTTGGAAGTTGACTAT TTTAATGTCTGCCAGGAGTTCTAATCCTGCTCTGTTCCCTTTTCTCTCTTTGAAAGTCC TTCCTGGAGCCTGTGCCTATGTCACTGCAATTTTCAGGAGACATATTCAACTCCTGCT AGCAGGAGCAGTITCTGGCCAGAAGCACCAGCCTGCTGCCAGCGGGGGCAGCCCCTCATAG 2447 2447 ARAGED MRNA Homo sapiens calcium/calmodulin-dependent CAMMIG) mRNA, complete cds. GI:16755791 AF428261 AF428261.1 LOCUS ACCESSION VERSION 1681 1741 1801 1861 1861 1921 1981 2041 2101 2101 2161 2161 2221 2281 2281 2341 2341 1501 1561 1621 1621 1681 1741 1801 1921 1981 2041 2221 2401 2401 1501 1561 RESULT 3 AF428261 qq q g δ 셤 Dp Dp QQ g g δ g qq οy qq ò 임 ΩY δy QΥ ÓΫ δy Ω Óγ g δ g δ Dp δ δ

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                    Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [, foases 1 to 2464]
Schutte, B.C., Bjork, B.C., Coppage, K.B., Malik, M.I., Gregory, S.G., Scott, D.J., Brentzell, L.M., Watanabe, Y., Dixon, M.J. and Murray, J.C. Ppieliniary gene map for the Van der Woude syndrome critical region derived from 900 kb of genomic sequence at 1q32-q41 Genome Res. 10 (1), 81-94 (2000)
                                                                                                                                                            gamma
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Bjork,B.C., Watanabe,Y., Murray,J.C. and Schutte,B.C.
Characterization of the human ortholog of rat CaM Kinase I (CamKig) at 1q32-q41
Unpublished
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Bjork, B.C., Watanabe, Y., Murray, J.C.
Direct Submission
Submitted (05-0cr-2001) Genetics, Uni
Iowa City, IA 52242, USA
Location/Qualifiers
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Pred. No. 0;
0; Mismatches
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Isogai, T. and Yamamoto, J.

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail; genomicséhri, Or. jp. Teli 18-138-52-3986, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA library

Construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5. & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation; HRI and RAB.

[Location/Qualifiers]
Lono sapiens CDNA FLJ38394 fis, clone FEBRA2007534, moderately similar to CamKI-like protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                         Tanigami, A., Fujiwara, T., Shibahara, T., Goto, Y., Hirao, M., Shimizu, F., Wakebe, H., Ono, T., Hishigaki, H., Watanabe, T., Ozaki, K., Sugiyama, T., Irie, F., Otsuki, T., Satto, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens fetal brain cDNA to mRNA, clone_lib:FEBRA2
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/dev_stage="fetal"
/note="cloning vector: pWH
a 750 c 645 g 598
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Db 1535 GT(Qy 1419 GTC) Db 1595 GT(Oy 1479 TGC	25.5	1715	Qy 1599 CAC	Db 1775 CA(Qy 1659 CC		Oy 1719 TG 	OY 1779 TC	 	Qy 1839 GG	Db 2015 GG	Qy 1899 AA(Db 2075 AA	QY 1959 CT(2135	Qy 2019 ATC	0.00	2079	2255	6513	2315	Oy 2199 GT/ 	23/5		24.33	2495	Qy 2379 CC	11 Db 2555 CC	RESULT 5
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		CACTACTACCTE	CGGGGTGTCTAC	cesesterciae	AAATACCTACAT		CTTACCCCTGAA	CAGAATGGCATC	CAGAATGGCATC	GCCCAGAAACCC	GCCCAGAAACCC	TTGCTCTGTGGA 		AAGGAGGCIAC 	GACTTTATTTGC	GACTTATTTGC	TTGAGTCATCCC	TTGAGTCATCCC	AGCCTCCAGATC	AGCCTCCAGATC	GCTGTGGTGCAC	GCTGTGGTGCAC	GAGGTGGAGAAC	GAGGTGGAGAAC	GAGATCACCATC	GAGATCACCATC	CAATTACCCTGC	CAATTACCCTGC	CTGGTCAATGGC	CTGGTCAATGGC	222999229229 	GTCCTCCTACTGCTCTGAGCCCACACTCCTCAAAAAGGCCAACAAAAAAAA
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CCTCCTACTGCTCTGAGCCCACACTCCTCAAAAAGGCCAACAAAAAACAGAACTTCAA PAAGGGCTGCAAGGAATTCTTATCCTGGCCACAFGTCCTCCGFGCACACACCCAATGGA PTAACCTTGGAAGTTGACTATTTTAATGTCTGCCAGGAGTTCTAATCCTGCCTCTGTTC STITICICICCITGAAAGICCAGCACACCATTCITGICCTICCCCCAGITICCICGCCCI PCGGAGGTCATGGTACCAGTTAAAGCCAGTGGCAGCTCCCACTGCCGGGCAGGGCAGAC GGAGTCTGTCTCATTATGTGATTCCTGGAGCCTGTGCCTATGTCACTGCAATTTTCAGG NGAGCAAGTGGAGCAGGGCTTAGCAGGAGCAGTTTCTGGCCAGAAGCACCAGCTGCTG 2ACCGGGGCAGCCCCTCATAGGAGGCCCAGGAGGGAGCCCCAAGGCGTAGAAGCCTTGT GGTCTGTGCTGTTTGTCGTGAAAAGCTTAATGGGCTGGCCAGGCTGTGTCTCACCTTCTCC FGAATGACAGCAGCTCCCCATGGTGGTCTGCCTGTGAGCTCTTCAAGTTCTAATCCTT

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ACCACATGAGGAAGCTACACATGAACCTGCACAGCCCGGGCGTCCGCCCAGAGGTGGAGA 1072
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                      Length 1738
                      6
                                             5;
                       В
                  Score 1734.8;
Pred. No. 0;
0; Mismatches
                     70.98;
99.98;
                                  Best Local Similarity 99.9
Matches 1736; Conservative
                         Query Match
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Submitted (21-APR-1999) E-mail contact: humquery@sanger.ac.uk
Submitted (21-APR-1999) E-mail contact: humquery@sanger.ac.uk
This sequence was generated from cDNA clones isolated using
sequence from the bacterial clone 272L16 (AL023754) and EST data.
The EST sequences listed match this sequence with an identity of at
least 95% between the coordinates shown.
Purther information can be found at
http://www.sanger.ac.uk/HGP/Chr1/ Partial, experimentally
determined gene.
Sanger Centre name: 61272L16.C1.1.
                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST A1215131 from clone IMAGE:1925595"
          similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(1469, .1550,1553, .1723,1721, .1738)
/note="matches EST R05661 from clone 29500"
1484. .1736
HS272L161 1738 bp mRNA linear Human gene isolated from PAC 272L16, chromosome 1, calcium/calmodulin dependent protein kinases.
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//crganism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="1"

/map="1q32_1-32_3"

<1. 1448

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764. .842
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931. .1355
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1356. .1483
/number=11
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Mammalia; Eutheria;
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/number=4
451. 574
/number=5
575. .650
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651. .763
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/number=1
108. .236
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237. .311
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653. .777
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BC021840
MGC.
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Submitted (18-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                             GCTCCCTCCACATCAGCAGCAGCCTGGTGCCCATGCATCAGGGGTCCCTGGCCGGGC
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                        Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne. amgelom.tmc.edu
Gunaratne. Y.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
                                                                                                                                            Clone distribution: MGC clone distribution information can be for through the I.M.A.G. E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 41 Row: 1 Column: 13 This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene
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A Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
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/tissue_type="Eye, retina, mouse strain C57Bl\6"
/clone_lib="NATH_MGC_94"
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/note="Vector: pCMV-SPORT6"
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Pred. No. 0;
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510 527 570 587 630	647 690 707	750	810 827	870 887	930	990	1050 1067	1110	1170	1227	1287	1347	1407	1467	1527 1547
TTGTCGGCAGTGAAATACCTACATGAGAATGGCATCGTCCACAGAGACTTAAAGCCCGAA	CAAGATGGAGCAGAATGGAGTCATGTCCACAGCTTGTGGGACCCCAGGCTGGTGG AGAAGTGCTGGCCCAGAAACCCTACAGCAAGGCTGTGGAATGCTGGTGCTGGCG 	ATCACCTACATATTGCTCTGTGGATACCCCCGGTTCTATGAAGAAACGGAGTCTAAGCTT 	TTCGAGAAGATCAAGGAGGCTACTATGAGTTTGAGTCTCCATTCTGGGATGACATTTCT 	GAGTCAGCCAAGGACTTTATTTGCCACTTGCTTGAGAAGGATCCGAACGAGCGGTACACC	TGTGAGAAGGCCTTGAGTCATCCCTGGATTGACGGAAACACGGCCCTCCACCGGGACATC	TACCCATCAGTCAGCCTCCAGATCCAGAACTTTGCTAAGAGCAAGTGGAGGCAAGCC	TTCAACGCAGCAGCTGTGGTGCACCACATGAGGAAGCTACACATGAACCTGCACCAGCCCG	GGGGTCCGCCCAGAGGTGGAGAACAGGCCGCTGAAACTCAAGCCTCAGAAACCTCTAGA 1 	CCCAGCTCCCCTGAGATCACCATCACCGAGGCACCTGTCCTGGACCACAGTGTAGCACTC	CCTGCCCTGACCCAATTACCCTGCCAGCAGCCGCCGCCCCACTGCCCCTGGTGGC	AGGICCTCAACTGCCTGGTCAATGGCTCCCTCCACATCAGCAGCAGCCTGGTGCCCATG	CATCAGGGGTCCCTGGCCGCGGGCCCTGTGGCTGCTGCTCCAGCTGCCTGAACATTGGG	agcaraggaragtcctcctactgctctgagcccacactcctcraraaggccarcaaaaaa	CAGAACTICAAGTCGGAGGTCATGGTACCAGTTAAAGCCAGTGGCAGCTCCCACTGCCGG	GCAGGGCAGACTGGACTCTCATTATGTGATTCCTGGAGCCTGTGCCTATGTCACTG
451 468 511 528 571	588 631 648	691 708	751	811	871 888	931	991	1051	1111	1171	1228	1288 1308	1348	1408	1468
oy oy oy	90 A	oy op	Oy Dp	Qy	Qy Db	Oy Db	Oy Dp	Qy	O.Y D.D	Qy Db	Oy	Oy Dp	Oy Dp	Qy Dp	Qy Dp

AF428262 2427 bp mRNA linear ROD 07-NOV-2001 Mus musculus calcium/calmodulin-dependent protein kinase I gamma aF428262 II GI:16755793 2045 TGGCCAGGCTGTGTCACCTTCTCCAAGCAAAGCCATATGGAGCATCTACCCAGACTCCCA 1934 2114 2046 GGAGCACTCACAACTCCAGTCCGTCCTCCAGGATTAGCTTCCCACTGCACGAGACCCA 2105 2174 AAGTGGAATAGAAAGAAGTTCATGAGTAAGGGCTGCAAGGAATTCTTATCCTGGCCACAT 2233 2160 regresacradadadecrerenceraresacraterecerrerecerecreses 2234 GTCCTCCGTGCACACACCCAATGGAGTTAACCTTGGAAGTTGACTATTTTAATGTCTGCC 2293 2294 AGGAGTICTAATCCTGCCTCTGTTCCCTTTTCTCTTGAAAGTCCAGCACACCATTCT 2353 2354 TGTCCTTCCCCAGTTTCCTCGCCCTCCACCCTCCAGCTTCATGCTCAGTTGTGCT-T 2412 AGGGAGGAAGGCAGAGCAAGTGGAGCAGGGCTTAGCAGGAGCAGTTTCTGGCCAGAAGCA 1647 CICIGCACACACTCACTCCCACCTCTCAAGCCTCCAACCTCTTGGCCAGATTGGGCTCAT 1994 TAATGTCGTTGCCTGCCCATCTGCATGAATGACAGGCAGCTCCCCATGGTGGTCTGCCTG 2054 1528 CAATTTTCAGGAGACATATTCAACTCCTCTGCTCTTCCAAACCTGGTGTCTATCCGGCAG 1587 TCCAGGTCTCCCTGACCTGCCTGTCTATGCCCCACACCCTACGTGCCGTGGCTCTGTGC 1814 ACCTCATATATCCCTAATTAAGG------ATTCGGGGACTATTCCATGTCATCC TGAGCTCTTCAAGTTCTAATCCTTAACTCCAGGATTAGCTCCCAAGTGCGCTGAGACCCA AGAAGCCTTGTTGAAGCTGTGAGCAGGAGAAGCGGT--------GCCCACCAGCT DEFINITION 1588 1606 1824 1884 1935 1995 1995 2055 2220 2323 2378 1708 1755 1765 1815 1875 2269 2413 RESULT 7 AF428262 LOCUS qq οy g οy Op Oy Dp ò В Οy Dp δ g QΥ qq δy В οχ qq QΥ qq Qγ qq QΥ Ω φ g δ q οy q

ACCESSION VERSION KEYWORDS

810 826 886 930 946

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CCCAGCTCCCCTGAGATCACCATCACCGAGGCACCTGTCCTGGACCACAGTGTAGCACTC 1170
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                                                                                                 GAGTCAGCCAAGGACTTTATTTGCCACTTGCTTGAGAAGGATCCGAACGAGCGGTACACC
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                                                TCCAAGATGGAACAGAATGGCATCATGTCCACTGCCTGTGGGACCCCAGGCTACGTGGCT
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           CGGATCCTAGAGCGTGGTGTCTACACAGAAAGGATGCCAGCCTGGTCATCCAGCAGGTC
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                                    TTGTCGCAGTGAAATACCTACATGAGAATGGCATCGTCCACAGAGACTTAAAGCCCCGAA
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         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 242)
Bjork, B.C., Watanabe, Y., Murray, J.C. and Schutte, B.C.
Characterization of the human ortholog of rat CaM Kinase I gamma
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                                                                                                                       Schutte, B.C
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1. .2427
                                                                                                 Unpublished
(2 (bases 1 to 2427)
Bjork,B.C., Watanabe,Y., Murray,J.C. and Direct Submission
Submitted (05-0CF-2001) Genetics, Univers
Iowa City, IA 52242, USA
Location/Qualifiers
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Pred. No. 0;
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                                                                                                                                                                                              /organism="Mus musculus"
/db_xref="taxon:10090"
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/clone="IMAGE:4502479"
/tissue_type="retina"
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                                                                                                                                                                                                                                                                                                 /gene="Camklg"
86. .1519
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1487 GGTGGGCAGACTGGGGTGTGTCTCGTTATGTGATCCCAGGAGCCCCATGTGGTTTTCAGGA 1546
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                           CAATTTTCAGGAGACATATTCAACTCCTCTGCTCTTCCAAACCTGGTGTCTATCCGGCAG 1587
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                                                    1547 GACATICCTG--GCTCTTCTCTGCCTCTCTGAGCTGGCATCTGCCCTGAGGAAGGGGGGC
                                                                                                                                    CCAGCCTGCTGCTGCCCAGCGCGCAGCCCCTCATAGGAGGCCCCAGGAGGCCCCAAGGCGGT
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HS272L16 bn linear PRI 23-NOV-1999 Human DNA sequence from clone 272L16 on chromosome 1432.1-32.3. Contains the 3' end of the LAMB3 gene for Laminin, Beta 3 (Nicein, Ralinin, BM600) and a novel Rat Ca2+/Calmodulin dependent Protein

RESULT 8 HS272L16 LOCUS DEFINITION

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Direct Submission

Loud Submitted (17-NOV-1998) Sanger Centre, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk CDIOnerequesf@sanger.ac.uk

On Dec 12, 1998 this sequence version replaced gi:3873472.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence is the entire insert of clone 272Li6. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272L16 is from the library RPCII constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: PCTPAC2 This sequence was generated from a human chromosome 1 bacterial clone contig constructed in collaboration by the Sanger Centre chromosome 1 mapping group and Brian Schutte, Bryan Bjork, Kevin Coppage and Jeffrey Murray. Department of Pediatrics, University of Iowa, USA. Further information can be found at http://www.sanger.ac.uk/HGP/Chri.
                                                                                                                                                                                                                                     Euteleostomi,
                                                                                         AL023754.1 GI:4007152
HTG; BM600; ca repeat polymorphism; Ca2+/Calmodulin dependent
Protein Kinase; D1S491; Kalinin; LAMB3; Laminin Beta 3; Nicein.
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/note="MLT1A2-internal repeat: matches 358. .1643 of
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/note="MLTIAl-internal repeat: matches 5. .450 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MLTIA2 repeat: matches 23. .374 of consensus"
3677. .4074
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2347. .2925
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/note="MSTD repeat: matches 1. .426 of consensus"
1585. .1875
/note="matches 1. .319 of consensus"
1898. .2024
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/note="LTR7 repeat: matches 1. .450 of consensus"
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Catarrhini; Hominidae; Homo.
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'note="MER54B repeat: matches 486. .902 of
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and a ca repeat polymorphism, complete sequence. AL023754
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6020. .6459
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="q32.1-32.3"
/clone="RPI-272116"
/clone="RPI-272116"
/clone="ib="RPCI-1"
966. .1078
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Mammalia; Eutheria; Primates;
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Grafham, D.
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64606781 /note="MMT1A1 repeat: matches 1318 of consensus"		/note="Mark repeat: matches 95146 of consensus 81508293	/note="MIR repeat: matches 68212 of c 83809083	/note= marko repear: matches 1/ll of consensus 90849303 /note="With reneat: matches 13	7493. 9493. sylvia repeat: matches 1. 304 of consensus	10108 . 10282	1092911005 /note="L2 repeat: matches 2671, .2748 of	. 12129 -"19 copies 2 mer ca 84% conserved"	12130 = 9 copies 4 mer acac 86% conser	repeat: matches 20	.13221 "MIR repeat:	complement(1356313979) /note="match: GSSs AQ075457 AQ076848" 14735 14737	#2333. note= 4327	· Σ	· 🗓 ·	/note="1	/note="L2 repeat: matches 17422 of consensus 1767917938	/note="MIR repeat: matches 7262 of consensus" 1789117953	/note="L2 repeat: matches 26942749 of consensus 1865018758	"L2 repeat: matches 26412750 of conse .19406	19871	/note="Lz repeat: matches 23092748 o 1991619987	="Mik repeat: matches 63140 of consensus" 2028	/NOTE="MEK34 repeat: matches 510, .538 of consensus 20233, .20365	/hote="MEK34 repeat: matches 413543 of consensus 2033820388	/note≈"LTR29 repeat: matches 454. ,503 of consensu: 2045920809	/note= 20976.	/note= 21834.	/note= 22477.	/note= 22826.	/not 2489	/note= 25084.	/note="M 25207.	/note="MIR
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Acote="WER4Az repeat: matches 1. .503 of consensus"

Acote="WER4Az repeat: matches 1. .503 of consensus"

Acote="WER4Az repeat: matches 1. .503 of consensus"

Acote="MITIF repeat: matches 1. .68 of consensus"

Acote="12 repeat: matches 2292. .2723 of consensus"

Acote="12 repeat: matches 2292. .2723 of consensus"

Acote="12 repeat: matches 2292. .2723 of consensus"

Acote="14 repeat: matches 4. .163 of consensus"

Acote="MAL1 repeat: matches 14. .355 of consensus"

Acote="MAL1 repeat: matches 355. .618 of consensus"

Acote="MAL1 repeat: matches 355. .618 of consensus"

Acote="MAL1 repeat: matches 355. .618 of consensus"

Acote="MAL1 repeat: matches 1189. .1455 of consensus"

Acote="MAL1 repeat: matches 1189. .1455 of consensus"

Acote="MAL1 repeat: matches 1125. .1189 of consensus"

Acote="MAL1 repeat: matches 3488. .6190 of consensus"

Acote="MAL1 repeat: matches 3488. .6190 of consensus"

Acote="MAL1 repeat: matches 3451. .4317 of consensus"

Acote="MAL1 repeat: matches 1. .300 of consensus"

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/note="Charliela repeat: matches 1. .1142 of consensus" 39293. .39437
/note="MIX repeat: matches 1. .140 of consensus" complement(39554. .39839)
/note="Match: GSS AQ070531"
41165. 41445
/note="L2 repeat: matches 2180. .2489 of consensus" 41615. .41810
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repeat: matches 68.
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                                ACATGTCCTCCGTGCACACCCAATGGAGTTAACCTTGGAAGTTGACTATTTAATGTC
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                                                                                                                                      147891 TCCCACTCTGCACACACTCCACCTCCTCAAGCCTCCAACCTCTTGGCCAGATTGGG
                                                                                                                                                             CTCATTAATGTCGTTGCCTGCCCATCTGCATGAATGACAGGCAGCTCCCCATGGTGGTCT
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                       TGTGCAGTGTACGTAGATAGCTCTCGCCTGGGTCTGTGCTGTTTGTCGTGAAAAGCTTAA
                                                                                                                TCCCACTCTGCACACACTCACTCCCACCTCTCAAGCCTCCAAACCTCTTGGCCAGATTGGG
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                                                                                                                           Craniata; Vertebrata; E
Sciurognathi; Muridae;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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D86557
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/ULATEL 1018-WORKEEDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRV
TGKLFALKGIKKSPAFRDSSLENEIAVLKRIKHENIVTLEDIYESTTHYYLVMQLVSG
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MITDFGLSKMEDNGYMGYMGTACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPP
FYEFTESKLFEKIKEGYFEFSFFWDDISESAKDFICHLLEKDPNERYTCEKALRHPW
TGGNTALHRDIYPSYSLQIQKNERAKSWRQAFN*

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                                                                                                                                                               /note="similar to calcium/calmodulin-dependent protein
kinase I mRNA (L24907, L26288)"
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Pred. No. 1.1e-213;
/db_xref="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="wr"
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                                     /clone="NS"
/tissue_type="brain"
/clone_lib="S. Nakanishi"
/dev_stage="embryo (E18)"
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                                                                                        AGCTGAAGAGAAGGCAACTGGCAAGCTCTTTGCTGTGAAGTGTATCCCTAAGAAGGCGCCT
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                           CCGGAAAACCTTCATTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTTTTCCT
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PWIAGDTALNKNIHESVSAQIRKNFAKSKWRQAFNATAVVRHMRKLHLGSSLDSSNAS
VSSLSLASCODCAYVARPESLS"
4 44 6 415 9 328 t
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Homo sapiens CamKI-like protein kinase mRNA, complete cds.
AF286366
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Identification and characterization of CKLiK: a novel granulocyte cast/calmodulin-dependent kinase
Blood (2000) In press
2 (bases 1 to 1579)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1579)
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Heidelberglaan 100, Utrecht 3584 CX, The
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                                                                                   GAGTCAGCCAAGGACTTTATTTGCCACTTGCTTGAGAAGGATCCGAACGAGCGGTACACC
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/protein_id="AAG00534.1"
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Pred. No. 3.2e-128;
0; Mismatches 274;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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88. .1161
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Direct Submission
Submitted (11-JUL-2000) Dept.
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Best Local Similarity 71.3%;
Matches 695; Conservative
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       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

Donoho,G., Scoville,J., Turner,C.A., Friedrich,G., Zambrowicz,B., Abuin,A. and Sands,A.T.

Novel human kinase proteins and polynucleotides encoding the same Patent: WO 0142435-A 5 14-JUN-2001;
Lexicon Genetics Incorporated (US)
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/db_xref="taxon:9606"
/ 437 c 448 g 333
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Ploman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Marti Flanagan, P. and Clary, D.S.
Novel human protein kinases and protein kinase-like enzymes Sugen, Inc. (US)
               AAAACCTTCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTTTTCCTGGTG
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Pred. No. 1.4e-127;
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/db_xref="taxon:9606"
258 c 276 g 22:
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AX166517
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71.3%;
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I (bases 1 to 1074)

Donoho,G., Scoville,J., Turner,C.A., Friedrich,G., Zambrowicz,B., Abuin,A. and Sands,A.T.

Novel human kinase proteins and polynucleotides encoding the same Patent: Wo 0142435-A 3 14-JuN-2001;
Lexicon Genetics Incorporated (US)
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                                             ATCATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGG---CATCATGTCCACT
                                                                                        GCCTGTGGGACCCCAGGCTACGTGGCTCCAGAAGTGCTGGCCCAGAAACCCTACAGCAAG
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Pred. No. 1.4e-127;
0; Mismatches 273;
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/db_xref="taxon:9606"
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AX167587
AX167587.1 GI:14596987
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Best Local Similarity 71.3%;
Matches 692; Conservative
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AAAACCTTCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTTTTCCTGGTG 189
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Donoho, G., Scoville, J., Turner, C.A., Friedrich, G., Zambrowicz, B., Abuin, A. and Sands, A. T.
Novel human kinase proteins and polynucleotides encoding the same Patent: Wo 014245-A 1 14-UNN-2001;
Lexicon Genetics Incorporated (US)
Location/Qualifiers
          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Cararrhini; Hominidae; Homo.
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Pred. No. 1.4e-127;
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SDFGLSKMEDPGSVLSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPF
YDBDDAKTEDQILKABYEBEDSFWNDDISDSARDPIRHUMEKDPEKRFTCEQALQHPWI
AGDTALDKNIHQSVSBOIKKNFARSKWKQAFNATAVKHMRKLQLGTSQEGGGTASH
GELLITPTAGGPAAGCCCRDCCVEPGSELPPAPPPSSRAMD"
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LVAIKCIAKKALEGKEGSMENEIAVLHKIKHPNIVALDDIYESGGHLYLIMQLVSGGE
LFDRIVEKGFYTERDASRLIFQVLDAVKYLHDLGIVHRDLKPENLLYYSLDEDSKIMI
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Rattus norvegicus
Ebkaryota, Metazoa; Chordata; Craniata; Vertebrata; Eute Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mux
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/tissue_type="lung"
/dev_stage="fetal"
/tissue_lib="day 21 gestation lung of 118. .1242
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/protein_id="AAA66944.1"
/db_xref="G1:439614"
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Pred. No. 5.2e-125;
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/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
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                                                                   380 GGGGCCACCTCAACCTCATGCAGCTGGTTTCAGGTGGAGAGCTGTTTGACCGAATG 439
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                                                           CCACCCACTACTACCTGGTCATGCAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCC
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Search completed: March 14, 2003, 17:25:23 Job time: 7400 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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March 14, 2003, 17:36:01; Search time 328 Seconds (without alignments) 3268.144 Million cell updates/sec Run on:

US-09-960-643-2 Title:

1 MGRKEEDDCSSWKKQTTNIR......VKASGSSHCRAGQTGVCLIM 476 Perfect score: Sequence:

Scoring table:

0.5 7.0 7.0 BLOSUM62 Xgapop 10.0, Xgapext (Ygapop 10.0, Ygapext (Fgapop 6.0, Fgapext Delop 6.0, Delext 2185239 seqs, 1125999159 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

MODEL=frame+_prim.mcdel -DEV=x1h
-Q=\coprol_tx299506643_trunat_07032003_090517_19867/app_query.fasta_1.647
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-LOSPEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -UOCALIGN=200 -THE_XCORE=E-pet -THE_MIN-0 -ALIGNS=15
-UOSEN-050960643_CGCN_11_263_CHUMAX-100 -THE_MIN-0 -ALIGNS=15
-UOSEN-050960643_CGCN_11_263_CHUMAT_07032003_090517_19867 -NCPU=6 -ICPU=3
-NOX_LDXI -NO_MANP -LARGEOURRY -NGC_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THERADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

Database :

/SIDS2/gcgdata/geneseg/genesegn-embl/NA1989.DAT:*/SIDS2/gcgdata/geneseg/genesegn-embl/NA1990.DAT:*/SIDS2/gcgdata/geneseg/genesegn-embl/NA1991.DAT:* /SIDS2/gcgdata/geneseg/genesegn-embl/NA1994.DA:* /SIDS2/gcgdata/geneseg/genesegn-embl/NA1995.DAT:* /SIDS2/gcgdata/geneseg/genesegn-embl/NA1996.DAT:* /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:* /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:* /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:* N_Geneseq_101002:* 15: 116: 117: 119: 220: 223: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseg/genesegn-embl/NA1999.DAT:*/SIDS2/gcgdata/geneseg/genesegn-embl/NA2000.DAT:*/SIDS2/gcgdata/geneseg/genesegn-embl/NA2000.DAT:*/SIDS2/gcgdata/geneseg/genesegn-embl/NA2001A.DAT:*/SIDS2/gcgdata/geneseg/genesegn-embl/NA2002.DAT:*/SIDS2/gcgdata/geneseg/genesegn-embl/NA2002.DAT:*

/SIDS2/gcgdata/geneseqn-embl/NA1997.DAT:*/SIDS2/gcgdata/geneseqn-embl/NA1998.DAT:*/SIDS2/gcgdata/qeneseqn/neneseqn-embl/NA1998.DAT:*

					SUMMARIES	
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! !	251	0.00	1956	22	AAI60703	uman polynucle
7	2513		4	24	AAD36140	
æ		φ.	16	22		Human polynucleoti
4	2327.5	95.6	2689	22	AAS31014	diagnos
3		σ.	73	22	AAD18817	Human kinase (PKIN
9	1246	φ.	07	22	AAS06708	Polynucleotide seq
7	1246	φ.	07	22	AAH25119	
80	1246		12	22	AAH25118	
6	1246	6	26	24	ABL60905	CaM ki
10	1246		99	22	AAD18826	Human kinase (PKIN
11	1246	6	67	22	AAH25120	Nucleotide sequenc
12	1246	δ.	16	22	AAI60424	
13	П	6	73	22	AAI58638	Human polynucleoti
14	1238.5	6	3	22	AAC90432	
15	_		7	22	AAD04775	Human death domain
16	1150.5	'n.	\sim	21	AAZ46162	cDNA sequence enco
17	1070		10	13	AAV18867	Calmodulin-depende
18	1041	Ϊ.	3	22	AAS06711	Polynucleotide seq
19	1036	ä	$\overline{}$	23	AAS70157	O
20	066	6	α	20	AAX06835	Disease associated
21	957.5	80	S	23	ABL02719	Drosophila melanog
22	753	0	0	22	AAK94614	Human full-length
23	753	0	-	22	AAI58143	
24	753	0	S.	22	AAF30481	Human protein phos
25	753	0	\circ	22	AAK94325	Human full-length
56	747.5	6	α	22	AAH78261	tide s
27	747.5	9	_	22	AAD18832	
28	747.5	σ.	2	24	ABA95682	
29	747	6	**	22	4	
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31	726.5	ω.	^	22	AAH99632	₽ .
32	683.5	7	^	53	'n.	encoding
33	683.5	ż	^	23	AAS90919	encoding
34		ė.	9	23	AAS66250	coding r
32		ė.	^	18	AAT71761	PSKH-1 CDNA. HOMO
36		9	1764	23	AAS64534	~
37		5	ထ	22	AAK52586	
38		5.	ഗ	22	AAK51602	Human polynucleoti
39		5	S	24	ABL40502	Human serine/threo
40		δ.	9	24	AAD34311	Human PKIN-14 cDNA
41		4.	0	24	ABL40503	Human serine/threo
42		4	\vdash	21	AAZ46160	cDNA sequence enco
43	611.5	24.3	1803	22	AAH46903	g
44		4.	0	24	38	kinase
45		4	a	24		Human ovary specif

ALIGNMENTS

AA160703 standard; cDNA; 1956 AA160703; AAI60703

RESULT 1

BP

(first entry) 22-OCT-2001

Human polynucleotide SEQ ID NO 4692.

Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

leukaemia; ss

Homo sapiens

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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM4213) with nootropic, the encoded polypeptides (AAM3642-AAM4213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous is system classed neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral scherosis, and Shy Darager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotextic/chemokinetic activity, haemostatic and thrombolytic activity, chemotextic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and c.N.S disorders.
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Zhang J;
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Yang Y,
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Xue AJ,
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Wehrman T,
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Wang Z, W
Zhou P,
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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                   (HYSE-) HYSEQ INC.
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           WO200153312-A1
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
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Wang J, W
Zhao QA,
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245 CGGGACAGCAGCCTGGAGAATGAGATTGCTGTTGAAAAAGATCAAGCATGAAAACATT
                                                                  AspCysTrpSerIleGlyValIleThrTyrIleLeuLeuCysGlyTyrProProPheTyr
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           SerLeuValIleGlnGlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIleVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for screening biologically active agent that modulates cancer associated protein kinase function. The invention also relates to a method for diagnosing cancer comprising determining the upregulation of expression of a nucleic acid sequence encoding a protein kinase. The method is useful for diagnosing cancer. A protein kinase is useful for screening biological agents that modulate cancer associated protein kinase function. Downregulating the activity of protein kinase is useful for inhibiting the growth of a cancer cell, e.g. liver or colon cancer. A nucleic acid encoding protein kinase is useful to screen biopsy cancer. A nucleic acid encoding protein kinase is useful to screen biopsy cancer. A nucleic acid encoding protein kinase is useful to screen biopsy amplified DNA in the cell or increased expression of corresponding mRNA amplified DNA in the cell or increased expression of corresponding mRNA such as molecular weight, amino acid and nucleotide sequences between the two cells. The present sequence is human calmodulin kinase CAMK-XI gene corresponding naced and cancer calmodulin kinase CAMK-XI gene corresponding protein chromosome 1932.1-32.3.
                                                                                                                                                                                                                                                       Human; cytostatic; antisense gene therapy; screening; protein kinase;
cancer; liver; colon; tumour; inflammation; arthritic synovium; CAMK-X1;
calmodulin kinase; enzyme; gene; chromosome 1q32.1-32.3; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosing cancer, comprises determining the upregulation of expression of a nucleic acid sequence encoding a protein kinase or upregulation of expression of the protein kinase, in the cancer
             1385 AAAAAGGCCAACAAAAAAAACTTCAAGTCGGAGGTCATGGTACCAGTTAAAGCCAGT
LysLysAlaAsnLysLysGlnAsnPheLysSerGluValMetValProValLysAlaSer
                                                    other;
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P-PSDB; AAE22764.
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Zhang J;
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Yang Y,
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, Xu C, Xue AJ,
R, Drmanac RT;
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Wehrman T, Xu
Goodrich R,
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2000US-0552317.
2000US-059042.
2000US-0653450.
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03-AUG-2000;
14-SEP-2000;
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09-JUL-2000;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system contains and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombulate activity, chemotextic/chemokinetic activity, nemostatic
                                                                                                                                                                                                                                                                                                                                                                                 and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S. disorders. Note: The sequence data for this patent did not form part of the printed Note:
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Conservative:
Mismatches:
Indels:
                                                         Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
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2001-442253/47.
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Best Local Similarity:
                                                                                                                      Claim 1; SEQ ID
                   P-PSDB; AAM39761
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Human diagnostic and therapeutic polynucleotide (DITHP) #29
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                                                                                                                                                                                     MetValProValLysAlaSerGlySerSerHisCysArgAlaGlyGlnThrGlyValCys
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                                                                                                    HisProTrplleAspGlyAsnThrAlaLeuHisArgAspIleTyrProSerValSerLeu
                                                                                                                       GlnIleGlnLysAsnPheAlaLysSerLysTrpArgGlnAlaPheAsnAlaAlaAlaVal
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The invention relates to polynucleotides (I) encoding diagnostic and therapeutic (DTHP) polypeptides (II), which include e.g. enzymes, and proteins involved in growth and development and receptors. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate DTHP expression. For example, (I) and (II) may be used to treat disorders associated with decreased polypeptide expression by rectifying mutations or deletions in a patient's genome,
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, Daffo A;
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                          leukaemia;
Human; receptor; diagnostic; therapeutic; gene therapy; vaccine cell proliferative disorder; Crohn's disease; lymphoma; leukaem acquired immune deficiency syndrome; AIDS; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang Chen A, D'Sa SA, Amshey S, Dahl CR, Dam TC, Daniels SE; Dufour GE, Flores V, Fong WT, Greenawalt LB, Hillman JL, i. Liu TF, Roseberry AM, Rose BH, Russo FD, Stockdreher TK, Waright RJ, Yap PE, Yu JY, Braddey DL, Bratcher SR, Chen W. Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;
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2000US-0184770.
2000US-0184771.
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17-MAY-2000;
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that affect the activity of the DITHPS, by expressing inactive proteins or supplementing the patient's own production of them. (1) and (II) may be used to treat disease, for example, cell proliferative disorder, crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma, leukaemia, autoimmune disorders, and respiratory disorders. Additionally, (I) may be used to produce the DITHPS, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies against DITHPP and in assays to identify modulators of DITHPP expression and activity. The anti-DITHPP antibodies and antigonists may also be used as diagnostic agents for detecting the presence of DITHPP in samples (e.g. by eazyme linked immunosorbant the presence of DITHPP in Samples (e.g. by eazyme linked immunosorbant and activity. The anti-DITHP imman diagnostic and the presence of DITHPP and antibodies and antibodies may also be used as diagnostic agents for detecting the presence of DITHPP in Samples (e.g. by eazyme linked immunosorbant and activity.) AASJ1196 represent human diagnostic and therapeutic (DITHP) polynucleotides of the invention. 82888888888888888888888888

Sequence 2689 BP; 642 A; 748 C; 678 G; 621 T; 0 other;

Length:
Matches:
Conservative:
Mismatches: Gaps: 7.06e-190 2327.50 95.86% 95.24% Percent Similarity: Best Local Similarity: Query Match: DB: .gnment Scores: .. 9

US-09-960-643-2 (1-476) x AAS31014 (1-2689)

356 416 476 100 536 40 9 80 ArgAspSerSerLeuGluAsnGluIleAlaValLeuLysLysIleLysHisGluAsnIle LysThrPheIlePheMetGluValLeuGlySerGlyAlaPheSerGluValPheLeuVal CGGGACAGCAGCCTGGAGAATGAGATTGCTGTGTTGAAAAAGATCAAGCATGAAAACATT ValThrLeuGluAspIleTyrGluSerThrThrHisTyrTyrLeuValMetGlnLeuVal _ 237 297 41 157 117 21 61 81 셤 셤 ద à ò ò 요 à ò

SerLeuValIleGlnGlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIleVal 140 101 477 537 121 셤 ŏ g ò

MetlleThrAspPheGlyLeuSerLySMetGluGlnAsnGlyIleMetSerThrAlaCys 141 657 161 유 ò õ

836 GlyThrProGlyTyrValAlaProGluValLeuAlaGlnLysProTyrSerLysAlaVal GGGACCCCAGGCTACGTGGCTCCAGAAGTGCTGGCCCAGAAACCCTACAGAAGGCTGTG ATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGGCATCATGTCCACTGCTGT 717 181 777

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AspCysTrpSerIleGlyValIleThrTyrIleLeuLeuCysGlyTyrProProPheTyr

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1136 1196 1316 TGTCCTGGACCACAGTGTAGCACTCCCTGCCTCTGACCCAATATACCCTGCCCAGCATCG 1376 418 ysAlaSerGLy-SerSerHisCysArgAlaGLyGlnThrGLyValCysLeuIleMet 476 OVAlleuAspHisSerValAlaLeuProAlaLeuThrGlnLeu---ProCysGlnHisGl GATCCGAACGAGGGGTAACACTGTGAGAGGGCTTGAGTCATCCCTGGATTGACGGTAA sIleSerSerSerLeuValProMetHisGlnGlySerLeuAlaAlaGlyProCysGlyCy GATTGCTGGTCCATCGGCGTCATCACCTACATATTGCTCTGTGGATACCCCCCATTCTAT AspProAsnGluArgTyrThr-CysGluLysAlaLeuSerHisProTrpIleAspGlyAs 300 laLysSerLysTrpArgGlnAlaPheAsnAlaAlaAlaVal-HisHisMetArgLys LeuHisMetAsnLeuHisSer-ProGlyValArgProGluValGluAsnArgProProGl uThrGlnAlaSerGluThrSerArgProSerSerProGluIleThrIleThrGluAlaPr GluGluThrGluSerLysLeuPheGluLysIleLysGluGlyTyrTyrGluPheGluSer 1077 1317 1377 1557 1017 1137 1197 339 1257 378 1437 418 1497 438 458 221 897 957 261 280 320 359 398 g g q QQ ŏ g δ qq δ qq ŏ qq ŏ g δ q ò g δ qq δ ō δy δy δý g

standard; cDNA; 1736 18-DEC-2001 (first entry) AAD18817; AAD18817 RESULT 5 AAD18817

> 959 160 716 180 776 200

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Human kinase, PKIN; gene therapy; adenocarcinoma; immune disorder; gout; cancer; allergy; sarcoma; leukaemia; acquired immune deficiency syndrome; AIDS; Addison's disease; microbial infection; inflammation; osteoporosis; atherosclerosis; cardiovascular disease; myocardial infarction; anaemia; myasthenia gravis; cirrhosis; cataract; growth and development disorder; pulmonary embolism; Gaucher's disease; lipid disorder; lipid storage disease; Pick's disease; pary-Sachs disease; land disease; asthma; obesity; restorative therapy; cytostatic; immunomodulatory; antimicrobial; cardiovascular; antimiflammatory; vaccine; ss. Human kinase (PKIN)-2 cDNA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to human kinases (PKIN) and the nucleic acids encoding them. PKIN is used as vaccine and in gene therapy. PKIN is used in the prevention, diagnosis and treatment of diseases cancers, adenocarcinoma, leukaemia, sarcoma, immune disorder, Addison's disease, acquired immune deficiency syndrome (AIDS), anaemia, asthma, allergies, gout, microbial infections, cardiovascular disease and/or inflammation, myasthenia gravis, atherosclerosis, cirrhosis, osteoporosis, myocardial infarction, cataract, growth and development disorder, seizure disorder, pulmonary embolism, Gaucher's disease, Inpid disorder, inpid storage disease, pick's disease, Tay-Sacks disease, renal disease and obesity. PKIN may be used to treat disorders associated with decreased PKIN expression by rectifying mutations or deletions in a patient's genome that affect the activity of PKN by expressing inactive proteins or to supplement the patients own production of PKIN PKIN nucleic acids may be used to produce the PKIN polypeptide, by inserting the nucleic acids into a chost cell and culturing the cell to express the protein. PKIN nucleic acids and its complementary sequences may also be used as DNA probes in a chost can and seaves to detect and quantitate the presence of similar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yue H, Gandhi AR, Tribouley CM, Kearney L, Griffin JA, Nguyen DB;
Bandman O, Lu DAM, Lal P, Burford N, Khan FA, Walia NK, Yao MG;
Patterson C, Burrill JD, Marcus GA, Zingler KA, Recipon SA, Lu Y;
Policky JL, Thornton M, Tang YT, Hafalia A, Elliott VS, Baughn MR;
Walsh RT, Ramkumar J, Borowsky ML, Au-young J, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human kinases and nucleic acids, useful for preventing diagnosing and treating cancers, inflammation and immune disorders \boldsymbol{\cdot}
                                                                                                                                                                                                   /*tag= c
/product= "Mature human PKIN-2 protein"
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                                                                                                             "Human PKIN-2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 151-152; 166pp; English.
                                        Location/Qualifiers
159..1232
                                                                                                                                                                                                                                                                                                                                                                                                   20-APR-2000; 2000US-199021P.
28-APR-2000; 2000US-200226P.
05-MAY-2000; 2000US-20339P.
11-MAY-2000; 2000US-203505P.
18-MAY-2000; 2000US-205564P.
26-MAY-2000; 2000US-2075739P.
01-JUN-2000; 2000US-208795P.
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279..1229
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Walsh RT, Ran
Gururajan R;
Homo sapiens
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AAACTACACCTCGGCAGCAGCTGGACAGTTCAAATGCAAGTGTTTCGAGCAGCCTCAGT 1178
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                                                                  LysThrPheIlePheMetGluValLeuGlySerGlyAlaPheSerGluValPheLeuVal
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US-09-960-643-2 (1-476) x AAD18817 (1-1736)
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Length:
Matches:
Conservative:
Mismatches:
Indels:

1.22e-97 1250.50 62.85% 51.03%

Best Local Similarity:

Query Match:

Percent Similarity:

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Nucleic acids encoding human kinase polypeptides, useful for preventing
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Inappropriate kinase expression. For example, they may be used to treat cancers (especially cancers of haematopotetic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), immune related diseases (e.g. rheumatoid arthritis), neurological disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. dathana), inflammatory disorders (e.g. asthana), inflammatory disorders (e.g. asthana), infectious disease (e.g. HIV) and reproductive disorders (e.g. infertility). Additionally, polynucleotides encoding protein kinases may be used for gene therapy and as DNA probes in diagnostic assays.

The protein kinase polypeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify
                                                                          AASO6701-AASO6757 encode for novel human protein kinases #1-57. The novel protein kinases have been identified as members of the tyrosine or serine/threonine kinase (PTK and STK) families. The polynucleotides encoding protein kinases and the polypeptides may be used in the prevention, diagnosis and treatment of diseases associated with
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diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections -
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                                                                                                                                                                                                                                                                                                                                 modulators of protein kinase expression and activity
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                                              Example 1; Figure 1; 433pp; English.
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The present sequence encodes a kinase polypeptide. The kinase polynuclectides and polypeptides are useful in therapeutic, diagnostic and pharmacogenic applications. They are useful for the detection of mutant kinases, or inappropriately expressed kinases for the diagnosis of a disease or disorder. They are useful for screening for drugs (or high throughput screening of combinatorial libraries) effective in the treatment of symptomatic or phenotypic manifestations of that disease or disorder. The polynucleotide sequence is useful as a source of probes and primers, which can be used to screen libraries, isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaSerLeuValIleGlnGlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIle 139
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                                                                                                                                                               clones, and prepare cloning and sequencing templates.
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                                                                                                                        Novel isolated human kinase polynucleotide that shares structural similarity with animal kinases including calcium/calmodulin-dependent protein kinases and serine/threonine protein kinases, useful in therapeutics -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; kinase; human disease; human disorder;
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Alignment Scores:

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The present sequence encodes a kinase polypeptide. The kinase polynucleotides and polypeptides are useful in therapeutic, diagnostic and pharmacogenic applications. They are useful for the detection of mutant kinases, or inappropriately expressed kinases for the diagnosis of a disease or disorder. They are useful for screening for drugs (or high throughput screening of combinatorial libraries) effective in the treatment of symptomatic or phenotypic manifestations of that disease or disorder. The polynucleotide sequence is useful as a source of probes and primers, which can be used to screen libraries, isolate clones, and prepare cloning and sequencing templates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated human kinase polynucleotide that shares structural similarity with animal kinases including calcium/calmodulin-dependent protein kinases and serine/threonine protein kinases, useful in
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                                                                                                                                   GACTCTCCCTACTGGGATGACATCTCCGACTCTGCAAAAGACTTCATTCGGAACCTGATG
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Human kinase; PKIN; gene therapy; adenocarcinoma; immune disorder; gout; cancer; allergy; sarcoma; leukaemia; acquired immune deficiency syndrome; AIDS; Addison's disease; microbial infection; inflammation; osteoporosis; atherosclerosis; cardiovascular disease; myocardial infarction; anaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polypeptide human CaM kinase I 39.05 and polynucleotide encoding said polypeptide -
                                                                                                                                                                                                  CaM kinase I 39.05; nervous disease; arrhythmia;
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                                                                                                                                                                        Human Cam kinase I 39.05 polypeptide encoding cDNA
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Mismatches:
Indels:
Gaps:
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Matches:
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18..1085
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                                                                                         ABL60905 standard; cDNA; 1565
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1246.00
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73.15%
49.58%
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/product= '
                                                                                                                                               (first entry)
        LysLeuHisMet 322
                                  961 AAACTACACCTC 972
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                                                                                                                                              23-SEP-2002
                                                                                                                                                                                                                                             Homo sapiens
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                                                                            ABL60905
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myasthenia gravis; cirrhosis; cataract; growth and development disorder; setaure disorder; pulmonary embolism; Gaucher's disease; lipid disorder; lipid storage disease; Pick's disease; arg-Sacks disease; renal disease; obesity; restorative therapy; immunomodulatory; vaccine; cardiovascular; antimicrobial; cytostatic; antiinflammatory; asthma; ss.

sapiens HOMO

Location/Qualifiers 159..1226 /*tag= a Key

/product= "Human PKIN-11 protein"

WO200181555-A2

01-NOV-2001

2001WO-US12992 20-APR-2001;

28-APR-2000; 05-MAY-2000; 11-MAY-2000; 20-APR-2000;

2000US-202339P. 2000US-203505P. 2000US-205564P. 2000US-207739P. 26-MAY-2000; 18-MAY-2000;

(INCY-) INCYTE GENOMICS INC

2000US-208795P

01-JUN-2000;

Nguyen DB; K, Yao MG; n SA, Lu Y; Baughn MR; Yue H, Gandhi AR, Tribouley CM, Kearney L, Griffin JA, Nguy, Bandman O, Lu DAM, Lal P, Burford N, Khan FA, Walia NK, Ya Patterson C, Burrill JD, Marcus GA, Zingler KA, Recipon SA, Policky JL, Thornton M, Tang YT, Hafalia A, Elliott VS, Bauw Walsh RT, Ramkumar J, Borowsky ML, Au-young J, Hillman JL: Policky JL, Walsh RT, Ra Gururajan R;

WPI; 2001-611740/70. P-PSDB; AAE11777.

and Human kinases and nucleic acids, useful for preventing diagnosing treating cancers, inflammation and immune disorders -

Claim 5; Page 159; 166pp; English.

cids encoding them. PRIN is used as vaccine and in gene therapy. PRIN is used in the prevention, diagnosis and treatment of diseases cancers, adenoma, leukemaia, sarcoma, immune disorder. Addison's disease, adenomar, leukemaia, sarcoma, immune disorder. Addison's disease, adenomar, leukemaia, sarcoma, immune disorder, Addison's disease, court microbial infections, cardiovascular disease and/or inflammation, mysathenia gravis, atherosclerosis, cirrhosis, osteoporosis, myccardial infarction, cataract, growth and development disorder, ipid storage disease, Pick's disease, Tay-Sachs disease, renal disease and obesity. PRIN may be used to treat disorders associated with decreased PRIN expression by rectifying mutations or deletions in a patient's genome that affect the activity of PRIN by expressing inactive proteins or to supplement the patients own production of PRIN. PRIN nucleic acids may be used to produce the PRIN polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. PRIN nucleic acids and its complementary sequences may also be used as DNA probes in cliangnostic assays to detect and quantitate the presence of similar nucleic acid summan because and contract sequences in samples and therefore which patients may be not of restorative therapy. The present sequence is human PRIN-11 The present invention relates to human kinases (PKIN) and the nucleic acids encoding them. PKIN is used as warming and the nucleic

Sequence 1661 BP; 408 A; 452 C; 448 G; 353 T; 0 other;

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Length:
Matches:
Conservative:
Mismatches:
          2.79e-97
1246.00
85.49%
73.15%
                                  Percent Similarity:
Best Local Similarity:
Alignment Scores:
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                                                                                                                                                                                                    100 ValSerGlyGlyGluLeuPheAspArgIleLeuGluArgGlyValTyrThrGluLysAsp
                                                                                                                                                                                                                                                                                           120 AlaSerLeuValIleGlnGlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIle
                                                                                                                                                                                                                                                                                                                                     ValHisArgAspLeuLysProGluAsnLeuLeuTyrLeuThrProGluGluAsnSerLys
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                                                                                                                                                                                                                                                                                                                                                                                                                            179 AlaCysGlyThrProGlyTyrValAlaProGluValLeuAlaGlnLysProTyrSerLys
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                                                                                                                        219 AAGATCTTCGAGTTCAAAGAGACCCTCGGAACCGGGGCCTTTTCCGAAGTGGTTTTAGCT
                                                                                                                                                                                                                                   80 IleValThrLeuGluAspIleTyrGluSerThrThrHisTyrLeuValMetGlnLeu
                                                                                                                                                                                                                                                        399 ATTGTTGCCCTGGAAGACATTTATGAAAGCCCAAATCACCTGTACTTGGTCATGCAGCTG
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 Indels:
           Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluSerProPheTrpAspAspIleSerGluSerAlaLysAspPheIleCysHisLeuLeu 258
    GGCAAGGAAAGCAGCATAGAGAATGAGATAGCCGTCCTGAGAAAGATTAAGCATGAAAAT 406
                                                                                                                                                                                         ValHisArgAspLeuLysProGluAsnLeuLyrLeuThrProGluGluAsnSerLys 159
                                                                                              AlaSerLeuValIleGlnGlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIle
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                                                      107 ATTGTTGCCCTGGAAGACATTTATGAAAGCCCAAATCACCTGTACTTGGTCATGCAGCTG
                                                                                 ValSerGlyGlyGluLeuPheAspArgIleLeuGluArgGlyValTyrThrGluLysAsp
                                                                                                                                                                                                         AlaCysGlyThrProGlyTyrValAlaProGluValLeuAlaGlnLysProTyrSerLys
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                             IleValThrLeuGluAspIleTyrGluSerThrThrHisTyrTyrLeuValMetGlnLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes a kinase polypeptide. The kinase polynucleotides and polypeptides are useful in therapeutic, diagnostic and pharmacogenic applications. They are useful for the detection of mutant kinases, or inappropriately expressed kinases for the diagnosis of a disease or disorder. They are useful for screening for drugs (or high throughput screening of combinatorial libraries) effective in the treatment of symptomatic or phenotypic manifestations of that disease or disorder. The polynucleotide sequence is useful as a source of
                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated human kinase polynucleotide that shares structural similarity with animal kinases including calcium/calmodulin-dependent protein kinases and serine/threonine protein kinases, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346
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                                                                                                                                                                                                                                                                                                                           Zambrowicz
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274
60
97
91
                                                                                                         Nucleotide sequence of a human kinase polypeptide
                                                                                                                                  human disease; human disorder; ss
                                                                                                                                                                                                                                                                                                                           Friedrich G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 32; 32pp; English.
                                                                                                                                                                                                                                                                                                                           CA,
                            ВР
                                                                                                                                                                                                                                                                                                                           Turner
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                            AAH25120 standard; DNA; 1671
                                                                                                                                                                                                                                                                                               (LEXI-) LEXICON GENETICS INC
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1246.00
64.35%
52.79%
49.58%
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                                                                                (first entry)
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Sands AT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1671 BP;
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                                                                                                                                    Human; kinase;
                                                                                                                                                                                       WO200142435-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                         07-DEC-2000;
                                                                                                                                                                                                                                                                     07-DEC-1999;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3662-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
                                                                                                                                         Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                          1485 TCTACTAAAATATAAAAATTAGCCGGGTGTGGTGGCGAGCACCTGTAATGTCAGCTACTT 1544
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--GlyGlyArgSerLeuAsnCysLeuValAsn 394
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                                                                                                               ProCysGlyCysCysSerSerCysLeuAsnIleGlySerLysGlyLysSerSerTyrCys
                                                      GlySerLeuHisIleSerSerSerLeuValProMetHisGlnGlySerLeuAlaAlaGly
                                                                                                                                                                                                ----ThrLeuLeuLysLysAlaAsnLysLysGln 447
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Zhang J;
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Yang Y,
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Xu C, Xue AJ,
, Drmanac RT;
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such as central nervous system injuries
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Wehrman T, Xu
Goodrich R,
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J, Wang Z, W
QA, Zhou P,
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09-JUL-2000;
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lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                           The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGAGAAGCAACTGGCAAGCTCTTTGCTGTGAAGTGTATCCCTAAGAAGGCGCTGAAG 323
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotinetic; thrombolytic; drug screening; arthritis; inflammation;
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Zhang
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Yang Y,
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Drmanac RT;
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25-APR-2000; 2000US-0552317.
9-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653450.
19-CT-2000; 2000US-0653450.
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Wang Z,
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Wang J, W
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utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                      assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
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Best Local Similarity:
                                                                                           Sequence 1733 BP;
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The present sequence is the coding sequence for Murine Dendritic Cell Kinase 3 (MDCK-3). The protein encoded by the present sequence is useful for treating a variety of disorders listed in the disclosure of the specification, including autoimmune disorders, allergic reactions, myeloid or lymphoid cell deficiencies, wound healing and tissue repair and replacement, burns, incisions and ulcers, periodontal disease, inflammatory diseases, tumours and bacterial, viral or fungal infection. MDCK-3 is a member of the Ca2+/calmodulin-dependent kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel murine and human kinase nucleic acids useful for treating inflammations, infections, tumors, allergies, autoimmune diseases, and for stimulating or suppressing immune responses
                                                                                           1055 GGTGACACACCCTCAACAAAACATCCACGAGTCCGTCAGCGCCCAGATCCGGAAAAC 1114
                                                                                                                                                                                                                                                                                                                                           Murine; Dendritic Cell Kinase; MDCK-3; autoimmune disorder; allergy; wound healing; periodontal disease; inflammatory disease; tumour; infection; Ca2+/calmodulin-dependent kinase family; ss.
                                        GlyAsnThrAlaLeuHisArgAspIleTyrProSerValSerLeuGlnIleGlnLysAsn
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antiarthritt; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmological; gene therapy; immunodeficiency disease; Acquired immune deficiency syndrome.

AIDS: leukaemia; autoimmune disease; systemic lupus erythematosus; hyperproliferative disorder; neoplasm; ocerebrovascular disorder; cerebral ischaemia; angiogenesis; cardiovascular disorder; ocular disorder; corneal infection; degenerative disease; Alzheimer's disease; Parkinson's disease; ocular disorder; corneal infection; degenerative disease; SMA; apoptosis; spinal muscular atrophy; epithalial cell proliferation; infection; cancer; wound healing; skin aging; chemotaxis; HDPVZ91 clone; ss.
                                                                                                                                                                                                                                                                                                           1484
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                                                                                                                                                                                                                                         394
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                                                                                       359 ProValLeuAspHisSerValAlaLeuProAlaLeuThrGlnLeu
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syndrome (IndS), leukaemia) autoimmune diseases (e.g. systemic lupus erythematosus, rheumatoid arthritis), hyperproliferative disorders (e.g. nopplasms of the breast or liver), cerebroascular disorders (e.g. cardiac arrest), neurodegenerative diseases (e.g. Alzheimer's (e.g. cardiac arrest), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), ocular disorders (e.g. corneal infection), degenerative diseases (e.g. spinal muscular atrophy-SMA), cancer, aberrant apoptosis, disorders of the placenta or uterus and infections caused by bacteria, viruses and fungi. The DDCR proteins infections caused by bacteria, viruses and fungi. The DDCR proteins to prevent skin aging due to sunburn, to maintain organs before transplantation, to support cell culture of primary tissues, to regenerate tissues and in chemotaxis. The DDCR sequences are used in correcting aberrant cellular apoptosis by gene therapy.

The present sequence is human death domain-containing receptor (DDCR) cDNCR) cDNCR icone HDPVZ91 (ATCC NO: PTAB39).
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They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. The DDCR protech and its antibodies are used in the diagnosis and treatment of disorders such as immunodeficiency diseases (e.g., Acquired immune deficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 AspAspCysSerSerTrpLysLysClnThrThrAsnIleArgLysThrPheIlePheMet
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SUMMARIES

:	Description	Sequence 4, Appli	2,	Sequence 1, Appli	46,	7, A	Sequence 50, Appl	Sequence 189, App	~	Sequence 48, Appl	Sequence 49, Appl	Sequence 177, App	ρ	Sequence 7777, Ap	Sequence 1, Appli	Sequence 45, Appl	Sequence 5, Appli	6, 7	Sequence 43, Appl	Sequence 44, Appl
	1D	US-09-935-464-4	US-09-935-464-2	US-09-935-464-1	US-09-935-464-46	US-09-935-464-7	US-09-935-464-50	US-09-764-868-189	US-09-935-464-47	US-09-935-464-48	US-09-935-464-49		US-09-935-464-6	US-09-796-692-7777	0 US-09-817-181-1	US-09-935-464-45	0 US-09-971-118-5	0 US-09-971-118-6	US-09-935-464-43	US-09-935-464-44
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Query	Match	6.99	90.6	36.9	18.9	18.4	13.0	11.2	8.7	8.5	7.6	6.1	3.3	1.3	1.3	1.1	1.0	1.0	6.0	6.0
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9 US-10-114-893-103 Sequence 103, App Sequence 15, Appl 10 US-09-935-464-56 Sequence 56, Appl 9 US-09-935-464-56 Sequence 56, Appl 9 US-09-935-464-54 Sequence 57, Appl 9 US-09-935-464-54 Sequence 57, Appl 9 US-09-935-464-18 Sequence 57, Appl 9 US-09-935-464-18 Sequence 57, Appl 10 US-09-770-445-96 Sequence 57, Appl 10 US-09-770-445-96 Sequence 57, Appl 10 US-09-778-844-206 Sequence 57, Appl 10 US-09-985-675-8 Sequence 57, Appl 10 US-09-985-675-8 Sequence 67, Appl 10 US-09-985-675-8 Sequence 67, Appl 10 US-09-985-675-9 Sequence 57, Appl 10 US-09-985-675-1 Sequence 560, Appl 10 US-09-985-675-1 Sequence 57, Appl 10 US-09-985-675-1 Sequence 560, Appl 10 US-09-985-675-1 Sequence 57, Appl 10 US-09-985-675-1 Sequence 580, Appl 10 US-09-984-981-560 Sequence 580, Appl 10 US-09-984-981-981 Sequence 581, Appl 10 US-09-982-10-98 Sequence 582, Appl 10 US-09-982-10-98 Sequence 582, Appl 10 US-09-984-531-524 Sequence 624, Appl 10 US-09-984-531-524 Sequence 621, Appl	ALIGNMENTS 109-935-464-4 6quence 4, Application US/09935464 FEDEDATE INFORMATION: APPLICANT: Meyer, Joanne APPLICANT: Barrington Martin, Rory APPLICANT: Barrington Martin, Rory APPLICANT: Barrington Martin, Rory APPLICANT: Barrington NETHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NETHORS SUCH AS SCHIZOPHRENIA TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA FILE REFERENCE: 3322/14702 US CURRENT APPLICATION NUMBER: US/09/935,464 CURRENT PILING DATE: 2001-09-9 FRIOR FILING DATE: 2001-01-09 SOFTWARE: PATENTIN VETSION 3.0 EBNCTH: 1738 TIPE: DNO 4 LENGTH: 1738 TIPE: DNO 4 TIPE: DNO 4	66.9%; Score 1636; DB 9; Length 1738; 99.9%; Pred. No. 0; .ive 0; Mismatches 2; Indels 0; Gaps 0;	CTTCAACTCTGGAGGCAATGGGTCGAAAGGAAGAACATGACTGCAGTTCCTGGAAGAAAC 112 	agaccaccaacatccggaaaccttcatttttatggaagtgctgggatcaggagctttct 172
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	SULT 1 Sequence 4, Application US/0993 Sequence 4, Application US/0993 Publication No. US20030027153A1 GENERAL INFORMATION: APPLICANT: Meyer, Joanne APPLICANT: Meyer, Joanne APPLICANT: Parking Alexander TITLE OF INVENTION: METHODS AN TITLE OF INVENTION: METHODS AN TITLE OF INVENTION: DISORDERS FILE REFERENCE: 332/2/14702 US CURRENT FILING DATE: 2001-09- PRIOR FILING DATE: 2001-09- PRIOR FILING DATE: 2001-09- ROMERER OF SEQ ID NOS: 90 SOFTWARE: PALENTIN VETSION 3.0 LENGTH: 1738 TYPE: DNA ORGANISM: HOMO SAPIENS -09-935-464-4	Query Match Best Local Similarity Matches 1736; Conser	ACTCTGGA ACTCTGGA	ACCAACAT
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λά d	413	ACACAGAGAAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAATACCTAC 472
6 64 1	2 7	TGAGAATGGCATGGTCCACAGAGACTTAAAGCCGGAAAACCTGGTTTACCTTACCCTG 53
QY	533	AAGAGAACTCTAAGATCATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGGCA 592
Oy Db	593	TCATGTCCACTGCCTGTGGGACCCCAGGCTACGTGGCTCCAGAAAGTGCTGGCCCAGAAAC 652
Qy Db	653	CCTACAGCAAGGCTGTGGATTGCTGGTCCATCGGCGTCATCACCTACATATTGCTCTGTG 712
ò a	713	GATACCCCCGGTTCTATGAAGAAACGAGTCTAAGCTTTTCCAGAAGATCAAGGAGGGCT 772
b cy	773	ACTATGAGTTTGAGTCTCCGTTCTGGGATGACATTTCTGAGTCAGCCAAGGACTTTATT 832
oy Gp	833	GCCACTIGCTIGAGAAGGATCCGAACGAGCGGTACACCTGTGAGAAGGCCTTGAGTCATC 892
oy Dp	893	CCTGGATTGACGGAACACGGCCCTCCACCGGGACATCTACCCATCAGTCAG
oy Op	953	GCAAG
op Op	1013	ACCACATGAGGAAGCTACACATGAACCTGCACAGCCCGGGCGTCCGCCCAGAGGTGGAGA 1072
o o	1073	ACAGGCCGCCTGAAACTCAAGCCTCAGAAACCTCTAGACCCAGCTCCCCTGAGATCACCA 1132
oy Op	1133	TCACCGAGGCACCTGTCCTGGACCACAGTGTAGCACTCCCTGCCCTGACCCAATTACCCT 1192
P Q	1193	GCCAGCATGGCCGGCCCACTGCCCCTGGTGGCAGGTCCCTCAACTGCCTGGTCAATG 1252
Qy Dp	1253	GCTCCCTCCACATCAGCAGCAGCCTGGTGCCCATGCATCAGGGGTCCCTGGCCGCGGGC 1312
Oy Db	1313 1261	CCTGTGGCTGCTCCAGCTGCCTGAACATTGGGAGCAAAGGAAAGTCCTCCTACTGCT 1372

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APPLICANT: Meyer, Joanne
APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYC,
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILLE REFERENCE: 3322/14702 US1
CURRENT APPLICATION NUMBER: US 09/757,300
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR FILLING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin version 3.0
SEQ ID NO 2.
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           CCTCTGCTCTTCCAAACCTGGTGTCTATCCGGCAGAGGAGGAAGGCAGAGCAAGTGGAG 1612
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.9%;
Matches 1339; Conservative
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CRGANISM: Homo sapiens
US-09-935-464-2
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APPLICANT: Meyer, Joanne
APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrer, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSY
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 332/14/102 USJ
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
PRIOR FILING DATE: 2001-09
NUMBER OF SEQ ID NOS: 90
SOFTHARE: PATENTIN VERSION 3.0
SOFTHARE: PATENTIN VERSION 3.0
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Pred. No. (
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100.0%; Pre
0;
                                                Sequence 1, Application US/09935464 Publication No. US20030027153A1 GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: HOMO S
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US-09-935-464-1
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Pred. No. 4e-212;
0; Mismatches 1; Indels
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APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TTTLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAG
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/1H702 US1
CURRENT APPLICATION UNMBER: US/09/935,464
CURRENT FILNG DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-01-09
                                                                                                                                                                                                                  Sequence 7, Application US/09935464; Publication No. US20030027153A1; GENERAL INFORMATION:
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Matches 500;
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APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 322141702 US.
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-09-33
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin version 3.0
SEQ ID NO 46
LENGTH: 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 ITTTCCTGGTGAAGCAAAGACTGACTGGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 CACCTGCCTTCCGGGACAGCAGCCTGGAGATGAGATTGCTGTGTTGAAAAAGATCAAGC
                                                                              TGGAGTTAACCTTGGAAGTTGACTATTTTAATGTCTGCCAGGAGTTCTAATCCTGCCTCT
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100.0%; Pred. No. 4.7e-218;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 46, Application US/09935464 Publication No. US20030027153A1 GENERAL INFORMATION:
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); OTHER INFORMATION: n=a or
US-09-935-464-46
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Matches 462; Conservative
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ORGANISM: Homo sapiens
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| Db 148396 CTA 148398
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APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Joanne
APPLICANT: Parker, John Merry
APPLICANT: Parker, John Merry
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/14702 USJ
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
PRIOR PILING DATE: 2001-09
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin version 3:0
SED ID NO 47
LENGTH: 467
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                                                                                        DB 9; Le
3.7e-125;
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Pred. No. 1.6e-94;
0; Mismatches 2;
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                                                                          11.2%; Scc. 100.0%; Pred. No. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385 CCTGCCTTCCGGGACAGCAGCCTGGAGAATGAGA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 CCTGCCTTCCGGGACAGCAGCCTGGAGAATGAGA 274
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               CATION: (59)
CTHER INFORMATION: n equals a,t,g, or US-09-764-868-189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 47, Application US/09935464 Publication No. US20030027153A1 GENERAL INFORMATION:
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Best Local Similarity 99.4%;
Matches 312; Conservative
                                                                                                                             Matches 274; Conservative
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                                                                                          Query Match
Best Local Similarity
NAME/KEY: SITE
LOCATION: (59)
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US-09-935-464-47
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                                                                                  Sequence 50, Application US/09935464
Publication No. US20030027153A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bearington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TITLE OF INVENTION: USFORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/1H702 US1
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 09/757,300
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn Version 3.0
SEQ ID NO 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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Pred. No. 2.1e-147;
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100.0%; Pred. No. ...
... 0; Mismatches
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 189, Application US/09764868
Patent No. US20020168711A1
GENERAL INFORMATION:
481 GCCTGCCCATCTGCATGAATG 501
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SEQ ID NO 189
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Matches 319; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-935-464-50
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                                                                    US-09-935-464-50
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Sequence 177, Application US/09731872

Sequence 177, Application US/09731872

GENERAL INPORMATION:

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Dobert, Severin

TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS

FILE REFERENCE: 78.US3.REG

CURRENT PAPLICATION NUMBER: US/09/731,872

PRIOR APPLICATION NUMBER: US 60/169,629

PRIOR APPLICATION NUMBER: US 60/169,629

PRIOR FILING DATE: 2000-03-06

NUMBER: US 60/187,470

NUMBER OF SEQ ID NOS: 482

SEQ ID NO 177

SEQ ID NO 177
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                                                                                                                                                                                                                                                      Query Match 7.6%; Score 185; DB 9; 18est Local Similarity 100.0%; Pred. No. 3.4e-81; Matches 185; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.1%; Score 149; DB 10; Best Local Similarity 100.0%; Pred. No. 2.3e-63; Matches 149; Conservative 0; Mismatches 0;
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                                                                                                                                                                    NAME/KEY: misc_feature; OTHER INFORMATION: n=a or g or c or t/u US-09-935-464-49
  PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin version 3.0
SEQ ID NO 49
LENGTH: 356
                                                                                                           TYPE: DNA ORGANISM: HOMO sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: 65..1024
US-09-731-872-177
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||GCTTG 330
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                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                                                         Sequence No. US20030027153A1

Sequence No. US20030027153A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Barrington-Martin, Rory
APPLICANT: Alexander
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 332/14/102 US1
CURRENT FILING DATE: 2001-08-23
PRIOR PILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin version 3.0
IENGTH: 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 49, Application US/09935464
Publication No. US20030027153A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mayer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIP
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REPRENEUR: 3322/14702 US1
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
181 TGAAGTGCATCAAGAAGTCACCTGCCTTCCGGGACAGCAGCAGCTGNAGAATGAGATTGCTG 240
                                                           183 CCTGGTGAAGCAAAGACTGGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCACC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 AAACATTGTGACCCTGGAGGACATCTATGAGAGCACCACCACTACTACTGGTCATGCA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 CCTGGTGAAGCAAAGACTGACTGGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCACC 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 TGCCTTCCGGGACAGCCTGGAGAATGAGATTGCTGTGTTGAAAAAGATCAAGCATGA 302
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8.5%; Score 209; DB 9; Lr
Best Local Similarity 100.0%; Pred. No. 4.8e-93;
Matches 209; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature; OTHER INFORMATION: n=a or g or c or t/u US-09-935-464-48
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                                                                                                                                                                    CCCACTACTACCTG 314
                                                                                                                                             341 CCCACTACTACCTG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                 RESULT 9
US-09-935-464-48
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US-09-935-464-49
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Sequence 45, Application US/09935464
Publication No. US20030027153A1
GENERAL INFORMATION:
APPLICANT: Mayer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TILLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSY
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TENDER 1. Application US/09817181

Sequence 1, Application US/09817181

Sequence 1, Application US/09817181

Sequence 1, Application US/09817181

GENERAL INCORMATION: USOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/817,181

CURRENT APPLICATION NUMBER: US/09/817,181

CURRENT FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.3%; Score 32; DB 9; Length 474; Best Local Similarity 100.0%; Pred. No. 1.4e-05; Matches 32; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                   PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-04
PRIOR PILING DATE: 2000-08-04
PRIOR PILING DATE: 2000-08-07
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                582 CCCTACAGCAAGGCTGTGGATTGCTGGTCCAT 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 CCCTACAGCAAGCTGTGGATTGCTGGTCCAT 198
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                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LCCATION: (10)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LCCATION: (19)
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: n=A,T,C or G
US-09-796-692-7777
  PRIOR FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32; Conservative
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (20
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US-09-935-464-45
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                                                                                                                                                                                                                                                                                                  TYPE: DNA
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APPLICANT: Algate, Paul A.

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY

TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES

FILE REFERENCE: 2077.001200

CORRENT APPLICATION NUMBER: 05/196,692

CORRENT FILING DATE: 2000-03-01

PRIOR PAPLICATION NUMBER: 60/190,479

PRIOR PAPLICATION NUMBER: 60/200,545

PRIOR PAPLICATION NUMBER: 60/200,303

PRIOR PAPLICATION NUMBER: 60/200,779

PRIOR PALING DATE: 2000-04-28

PRIOR PALING DATE: 2000-04-28

PRIOR PALING DATE: 2000-04-28

PRIOR PAPLICATION NUMBER: 60/200,779

PRIOR PAPLICATION NUMBER: 60/200,779

PRIOR APPLICATION NUMBER: 60/200,999

PRIOR PAPLICATION NUMBER: 60/200,099

PRIOR PAPLICATION NUMBER: 60/200,099

PRIOR PAPLICATION NUMBER: 60/200,001

PRIOR PALING DATE: 2000-05-04

PRIOR PAPLICATION NUMBER: 60/200,201

PRIOR PAPLICATION NUMBER: 60/200,201

PRIOR APPLICATION NUMBER: 60/200,201

PRIOR APPLICATION NUMBER: 60/200,201

PRIOR APPLICATION NUMBER: 60/200,201

PRIOR APPLICATION NUMBER: 60/200,201
                                                                                                                                                                                                                                  APPLICANT: Meyer, Joanne
APPLICANT: Barrington Martin, Rory
APPLICANT: Barrington Martin, Rory
APPLICANT: Parker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/11702 US1
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
PRIOR FILING DATE: 2001-09
PRIOR FILING DATE: 2001-09
NUMBER OF SEQ ID NOS: 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CACTGCAATTITCAGGAGACATATICAACTCCTCTGCTCTTCCAAACCTGGTGTCTATCC 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: misc_feature
; OTHER INFORMATION: n = a or g or c or t/u
US-09-935-464-6
1297 ATGGACATATTTTCTCTAAAAAAAA 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7777, Application US/09796692 Publication No. US20020198362A1 GENERAL INFORMATION: APPLICANT: Gaiger, Alexander
                                                                                                                                US-09-935-464-6
; Sequence 6, Application US/09935464
; Publication No. US20030027153A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1583 GGCAGAGGGAGGAAGGCAGA 1602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.0 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 GGCAGAGGGAGGAAGGCAGA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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; FILE REFERENCE: 3322/1H702 US1
; CURRENT APPLICATION NUMBER: US/09/935,464
; CURRENT PAPLICATION NUMBER: US/09/935,464
; PRIOR PLICATION NUMBER: US 09/757,300
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patentin version 3.0
; TAPE: DNA
; FATURE: US.
; CONSETVARION: DNA probe
; CONSETVARION: DNA probe
; SOFTWARE: Patentin version 3.0
; Gaps 0;

QV 293 TCAAGCATGAAAACATTGTGACCCTGG 3.0
; Indels 0; Gaps 0;

AND 1 TCAAGCATGAAAACATTGTGACCTGG 2.0
; DD 1 TCAAGCATGAAAACATTGTGACCTGG 2.0
Search completed: March 15, 2003, 05:09:04
JOb time: 401 secs
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March 14, 2003, 14:03:36 ; Search time 38 Seconds
   (without alignments)
   1669.139 Million cell updates/sec
                                                                                                                                                                                                           US-09-960-643-2
2513
1 MGRKEEDDCSSWKKQTTNIR.....VKASGSSHCRAGQTGVCLIM 476
                                                                                                                                                                                                                                                                                                                                                                                                            908470
GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Database :

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| SIDSI/gcgdata/geneseqy-embl/Aa1982.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result		% Query				
No.	Score	Match	Match Length DB	DB	ID	Description
-	2513		476	23	AAE22764	Human calmodulin k
7	2513		497	22	AAM41547	Human polypeptide
e	2499.5	99.5	567	22	AAM39761	Human polypeptide
4	1382		298	22	AAU19443	Human diagnostic a
2	1246		355	22	AAE11777	Human kinase (PKIN
9	1246		355	22	AAM41268	Human polypeptide
7	1246		355	23	ABB08178	Human Cam kinase I
8	1246		357	22	AAE11768	Human kinase (PKIN
6	1246		385	22	AAM39482	Human polypeptide
10	1246		385	22	AAB84359	Amino acid sequenc

(KINE-) KINETEK PHARM INC. (UYBR-) UNIV BRITISH COLUMBIA.

Yoganathan T, Delaney AD;

2000US-237419P. 2000US-237423P. 2000US-238558P. 2001US-290555P.

02-0CT-2000; 02-0CT-2000; 04-0CT-2000; 10-MAY-2001; 20-SEP-2000;

2000US-233999P

20-SEP-2001; 2001WO-IB02237

28-MAR-2002

II:	1241	49.4	357	22	AAU03508	protein kin
7.5	17	49.I	355	7 (AAB50055	Dend
L3	٦,	49.0	356	77	AAB84360	ac1d
14 15	1145	٠. د	989	7.7	AAY68/93	Amino acid sequenc
7 -	> <	, v -	0 7 0	12	AAMOULUS AAHOSE11	Tumes protois kins
17	>		503	7 0	AA003311 ABG05970	Novel buren diagno
18	0		343	20	AAW88436	9886
13	57,	, α	405	22	ABB58176	Drosophila melanog
20	44	7.	280	22	AAE01034	Human death domain
21	47	9.	501	22	AAE11783	kinas
22	747.5	٠ م	501	22	AAG67539	
23.0	4 4 - 4		20T	2 6	AAM482/9	Human protein Kina
25	4 4	· 0	470	25	AAM93404	
26	4.5		470	22	AAM93679	
27	45	6.	470	22	AAB20327	Human protein phos
28	\sim	6	470	22	AAM38987	
29	m	6	501	22	AAM93379	Human polypeptide,
30	vo.	ω.	205	22	AAM25691	
31	691.5	۲.	502	21	AAY54580	A rat calcium/calm
33	\sim		474	22	AAM10244 AAM79453	٦ ,
34) r	` .	444	200	AAM78469	protein
35	່ວ	, L	449	22	ABG00347	human di
36	ועו	4	992	23	AAE21719	PKIN-14
37	מנ	4	992	23	AAG66161	serine/t
38	(O)	4.	264	20	AAY43925	prote
6 K	615.5	24.5	641	21	AAY68791	acid seq
7 7		* =	000	7 0	AAB00000	procein
4.7	-) v	• =	474	2 5	AAE2414/ ABG02063	Movel buman diagno
43	99	. m	493	22	ABB65515	Drosophila melanog
44	599.5	٠. م	493	22	ABB66655	Drosophila melanog
45	99	23.9	493	22	ABB66656	Drosophila melanog
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RESULT	1					
AAE22764	4					
ID AA	AAE22764 st	standard;	Protein		476 AA.	
	AAE22764;					
	C00C-D114-00			;		
20 27	-AUG-200.	Z (IIISL	- encry	χ)		
	Human calmo	calmodulin kinase,	Inase,		CAMK-X1.	
KW Hu KW Ca KW en	Human; cytc cancer; liv enzyme; cal	cytostatic; antise liver; colon; tum calmodulin kinase	C	tisense tumour; nase.	gene therapy; screening; ; inflammation; arthritic	; protein kinase; c synovium; CAMK-X1;
	Homo sapiens	ns.				
	WO200224947-A2	7-A2.				

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                                                                                                                                  that modulates cancer associated protein kinase function. The invention also relates to a method for diagnosing cancer comprising determining the upregulation of expression of a nucleic acid sequence encoding a protein kinase. The method is useful for diagnosing cancer. A protein kinase is besful for screening biological agents that modulate cancer associated protein kinase function. Downregulating the activity of protein kinase is useful for inhibiting the growth of a cancer cell, e.g. liver or colon cancer. A nucleic acid encoding protein kinase is useful to screen biopsy derived tumours and inflammatory samples such as arthritic synovium, for amplified DNA in the cell or increased expression of corresponding mRNA or protein and is also useful to detect differences in expression levels such as molecular weight, amino acid and nuclectide sequences between the two cells. The present sequence is human calmodulin kinase, CAMK-XI.
                                                                                                                        The invention relates to a method for screening biologically active agent
                                       comprises determining the upregulation of expression sequence encoding a protein kinase or upregulation of
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                                                                                                                                                                                                                                                                                                                                                        ; Score 2513; DB 23; Length 476;
; Pred. No. 4.8e-220;
0; Mismatches 0; Indels 0;
                                                   of a nucleic acid sequence encoding a protein ki
expression of the protein kinase, in the cancer
                                                                                           Claim 1; Page 64-65; 87pp; English.
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100.0%;
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Matches 476; Conservative
2002-394145/42
                                         Diagnosing cancer,
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           N-PSDB; AAD36140
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with noctropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, asch as peripheral nervous injuries, peripheral nervous system, as and and localised neuropathies and central nervous system diseases, aumoir ophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and constants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptides, useful for treating disorders system injuries -
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Zhang J;
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Yang Y,
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100.0%; Pred. No. 5.1e-220;
ive 0; Mismatches 0;
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Xu C, Xue AJ,
R, Drmanac RT;
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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13-NG-2000; 2000US-0653450.
14-SEP-2000; 2000US-06534519.
19-CCT-2000; 2000US-0639336.
29-NOV-2000; 2000US-0727344.
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2000US-0598042.
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Matches 476; Conservative
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
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Wang
Zhao
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide
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 GTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFES
                                           PFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFA
                                                      LDHSVALPALTQLPCQHGRRPTAPGGRSLNCLVNGSLHISSSLVPMHQGSLAAGPCGCCS
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J,
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Zhang
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Yang Y,
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Drmanac RT;
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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2000US-0552317.
2000US-0598042.
2000US-063450.
200US-0653450.
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2000US-0653450.
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14-SEP-2000;
19-OCT-2000;
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09-JUL-2000;
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Zhao QA,
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peripheral nervous
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                                                                                                                                                                                                                                                                                                                        Human; receptor; diagnostic; therapeutic; gene therapy; vaccine; cell proliferative disorder; Crohn's disease; lymphoma; leukaemia; acquired immune deficiency syndrome; AIDS; autoimmune disorder;
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used to treat diseases of the
                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                99.5%; Score 2499.5; DB 2 98.6%; Pred. No. 1.1e-218;
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the invention may
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AAE11777 standard; Protein; 355
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99.3%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the invention relates to polynucleotides (I) encoding diagnostic and therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, and proteins involved in growth and development and receptors. (I) and proteins involved in the prevention, diagnosis and treatment of diseases associated with inappropriate DITHP expression. For example, (I) and expression by rectifying mutations or deletions in a patient's genome, that affect the activity of the DITHPs, by expressing inactive proteins or supplementing the patient's own production of them. (I) and (II) may be used to treat diseases, for example, cell proliferative disorder. Crohn's disease, acquired immune deficiency syndrome (AIDS). Immphoma, leukaemia, autoimmune disorders, and respiratory disorders. Additionally, (I) may be used to produce the DITHPs, by inserting the nucleic acids into a host call and culturing the cell to express the protein. (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones AL;
, Daffo A;
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                                                                                                                                                2000US-0184772.
2000US-0184773.
2000US-0184774.
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2000US-0185216.
2000US-0203785.
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Dufour GE, Florecomer. Roseberry AM,
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WO200162927-A2.
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24-FEB-2000;
24-FEB-2000;
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16-MAY-2000;
16-MAY-2000;
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17-MAY-2000;
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17-MAY-2000;
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24-FEB-2000;
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samples, and therefore which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies against DITHPs and in assays to identify modulators of DITHP expression and activity. The anti-DITHP antibodies and antaqonists may also be used to down regulate expression and activity. The anti-DITHP antibodies may also be used as diagnostic agents for detecting the presence of DITHPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAG19415-AAG19525 represent human diagnostic and therapeutic (DITHP) polypeptides of the invention.
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/note= "Tyrosine kinase catalytic domain"
202...224
/note= "Tyrosine kinase catalytic domain"
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Pred. No. 2.9e-117;
0; Mismatches 2;
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hote= "Protein kinase domain"
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                  leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                      cidis encoding them. PRIN is used as vaccine and in gene therapy. PRIN is used in the prevention, diagnosis and treatment of diseases cancers, adenova, learners, adenova, edisease, adenovar, learners, adenovar, disease, adenovar, learners, adenovar, disease, adenovar, learners, astema, allergies, cquired immune deficiency syndrome (AIDS), anaemia, asthma, allergies, gout, microbial infections, cardiovascular disease and/or inflammation, infarction, cataract, growth and development disease and/or inflammation, infarction, cataract, growth and development disease and obesity. PRIN may be used to treat disorders associated with decreased PRIN expression by rectifying mutations or deletions in a patient's genome that affect the activity of PRIN by expressing inactive proteins or to supplement the patients own production of PRIN PRIN mucleic acids may be used to produce the PRIN polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. PRIN nucleic acids and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic assays to detect and quantitate the presence of similar concleance of restorative therapy. The present sequence is human PRIN-11
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Baughn MR;
                                                                                                                                                                                                                                                                                                             useful for preventing diagnosing and immune disorders -
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                                                                                                                                                                                                                                                                                                                                                                                present invention relates to human kinases (PKIN) and the nucleic
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                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 137-138; 166pp; English.
                                                                                                                                                                                                                                                                                                             Human kinases and nucleic acids, us treating cancers, inflammation and
                                                              2000US-200226P.
2000US-202339P.
2000US-203505P.
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2000US-207739P.
2000US-208795P.
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                       20-APR-2001; 2001WO-US12992
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hes 237; Conservative
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11-MAY-2000;
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26-MAY-2000;
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the encoded polypeptides (AAMA21213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Sydrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and considered.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
241 DSPYMDDISDSAKDFIRNLMEKDPNKRYTCEQAARHPWIAGDTALNKNIHESVSAQIRKN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peripheral nervous system, neuropathy; central nervous system; CNS; Alzhehmer's; Parkinson's disease, Huntington's disease, haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for treating disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen R, Ma Y,
Xu C, Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; SEQ ID NO 6199; 10078pp; English.
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                                                                                                                                                                                                                                                                                                                        AA.
                                                                                              FAKSKWRQAFNAAAVVHHMRKLHM 322
                                                                                                                               301 FAKSKWRQAFNATAVVRHMRKLHL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polypeptide SEQ ID NO 6199.
                                                                                                                                                                                                                                                                                                                 AAM41268 standard; Protein; 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0693036
2000US-0727344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
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Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAI60424
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355 AA;
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28-APR-2000;
05-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
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                                                                                                                                                                                                                                                                                                                     AAE11768;
           Sequence
                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention discloses a novel polypeptide-human CaM kinase I 39.05, polynucleotide for coding the polypeptide and method for producing this polypeptide by DNA recombination technology. The polypeptide is useful for treating diseases such as nervous disease, arrhythmia, tumour and growth development disturbance disease. The present sequence represents the human CaM kinase I 39.05 polypeptide.
                                                                                                         61 GKESSIENEIAVLRKIKHENIVALEDIYESPNHLYLVWQLVSGGGLFDRIVEKGFYTEKD 120
                                                                                                                                 178
                                                                                                                                          238
                                                                                                                                                                                                      ESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKN 298
                                                                                                                                                                                                                60 FRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKD 119
                                            Gaps
                                                                     1 MGRKEEDDCSSWKKQTINIRKTFIFWEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPA 59
                                                                                                                                 ASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEONG-IMST
                                                                                                                                                                    ACGIPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEF
                                                                                                                                                                              Novel polypeptide human CaM kinase I 39.05 and polynucleotide for
encoding said polypeptide –
                                                                                                                                                                                                                                                                                                                                                                      Human; CaM kinase I 39.05; nervous disease; arrhythmia; tumour;
                                            ;;
                          Length 355;
                                            Indels
                       Score 1246; DB 22;
Pred. No. 9.4e-105;
); Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 27-28 (disclosure); 35pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                     Human Cam kinase I 39.05 polypeptide.
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                                                                                                                                                                                                                                                 FAKSKWRQAFNAAAVVHHMRKLHM 322
                                         40;
                                                                                                                                                                                                                                                                                                   ABB08178 standard; Protein; 355
                         49.68;
73.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUL-2000; 2000CN-0119405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-2000; .2000CN-0119405
                                                                                                                                                                                                                                                                                                                                    23-SEP-2002 (first entry)
                                        237; Conservative
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N-PSDB; ABL60905.
                                   Similarity
         A.
         355
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        Sequence
                         Query Match
Best Local
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                                           Matches
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ABB08178
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                                                                                                                                                                                                                                                 61 GKESSIENEIAVLRKIKHENIVALEDIYESPNHLYLVMQLVSGGELFDRIVERGFYTERD 120
                                                                                                                                                                                                                                                                                                                            ASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMST 178
                                                                                                                                                                                                                                                                                                                                                        FRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKN 298
                                                        Gaps
                                                                                                          1 MGRKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPA 59
                                                                                                                                         ACGTPGYVAPEVLAQKPYSKAVDCWS1GV1TY1LLCGYPPFYEETESKLFEK1KEGYYEF
                                                        2;
  Length 355;
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41..357
/label= Human_mature_PKIN-2_protein
                                                        Indels
; Score 1246; DB 23;
; Pred. No. 9.4e-105;
40; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Protein kinase domain"
23..279
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24..270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human kinase (PKIN)-2 protein.
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2000US-200226P.
2000US-202339P.
tch 49.6%; al Similarity 73.1%; 237; Conservative 4
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WPI; 2001-442253/47.
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Best Local Similarity
Matches 237; Conserv
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Wang Z, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 385 AA;
                                                                                                                                                                                                       nootropic;
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                                                                                                                                                                                                                                                                                                                                                                    WO200153312-A1.
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN-2000;
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                                                                                                                            22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                         26-JUL-2001
                                                                                                                                                                                                                                                                                               leukaemia.
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                                                                                            AAM39482;
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Zhao (
                   RESULT 9
                                      AAM39482
                                                                                          cids encoding them. PRIN is used as vaccine and in gene therapy. PRIN is used in the prevention, diagnosis and treatment of diseases cancers, adenovarionma, leukaemia, sarcoma, immune disorder, Addison's disease, adenovarcinoma, leukaemia, sarcoma, immune disorder, Addison's disease, adenovarcinoma, leukaemia, sarcoma, immune disorder, asthma, allergies, gout, microbial infections, cardiovascular disease and/or inflammation, mysthenia gravis, atherosclerosis, cirrhosis, osteoporosis, myocardial infarction, cataract, growth and development disorder, lipid storage disease, pick's disease, Tay-Sachs disease, Inpid disorder, lipid storage disease, pick's disease, Tay-Sachs disease, renal disease and obesity. PKIN may be used to treat disorders associated with decreased PKIN expression by rectifying mutations or deletions in a patient's genome that affect the activity of PKIN by expressing inactive proteins or to supplement the patients own production of PKIN PKIN moleic acids may be used to produce the PKIN polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. PKIN nucleic acids and its complementary sequences may also be used as DMA probes in call and its complementary sequences may also be used as DMA probes in nucleic acid sequences in samples and therefore which patients may be incorporated and acid sequences in samples and therefore which patients may be incorporated.
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                                                                                                     1 AR, Tribouley CM, Kearney L, Griffin JA, Nguyen DB, u DAM, Lal P, Burford N, Khan FA, Walia NK, Yao MG; Burill JD, Marcus GA, Zingler KA, Recipon SA, Lu Y; Thornton M, Tang YT, Hafalia A, Elliott VS, Baughn MR; mkumar J, Borowsky ML, Au-young J, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human kinases and nucleic acids, useful for preventing diagnosing and treating cancers, inflammation and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to human kinases (PKIN) and the nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GKESSIENEIAVLRKIKHENIVALEDIYESPNHLYLVWQLVSGGELFDRIVEKGFYTEKD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 FRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 ASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.6%; Score 1246; DB 22; 73.1%; Pred. No. 9.5e-105; tive 40; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 124-125; 166pp; English.
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2000US-205564P.
                                                                      (INCY-) INCYTE GENOMICS INC
                                                                                                               Yue ",
Bandman O, Lu Daw,
Patterson C, Burrill JD,
TT. Thornton M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 73.1
Matches 237; Conservative
                                                                                                                                                                                Ramkumar J,
                                                                                                                                                                                                                                      2001-611740/70.
                                                                                                         Gandhi AR,
O, Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 AA;
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18-MAY-2000;
                                                                                                                                                                                                 Gururajan R;
                                                                                                                                                             Policky JL,
Walsh RT, R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leukaemias and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang D;
                                                                                                                                                                                                                                                                                         peripheral nervous system; neuropathy; central nervous system; CNS; Alzhehmer's; Parkinson's disease; heamostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ren F, War
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.6%; Score 1246; DB 22; 73.1%; Pred. No. 1.1e-104; tive 40; Mismatches 45;
                                                                                                                                                                                                                                                             cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asundi V, Chen R, Ma Y,
Wehrman T, Xu C, Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; SEQ ID NO 2627; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for receptor activity, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT;
                                                                                                                                                                                                                                                                 immunosuppressant;
AAM39482 standard; Protein; 385 AA.
                                                                                                                                                                                         Human polypeptide SEQ ID NO 2627.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0488725.
2000US-055317.
2000US-0598042.
2000US-0620312.
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2000US-0693036.
2000US-0727344.
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                                                                                                                              (first entry)
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385 AA;

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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a kinase polypeptide. The kinase polynucleotides and polypeptides are useful in therapeutic, diagnostic and pharmacogenic applications. They are useful for the detection of mutant kinases, or inappropriately expressed kinases for the diagnosis of a disease or disorder. They are useful for screening for drugs (or high throughput screening of combinatorial libraries) effective in the treatment of symptomatic or phenotypic manifestations of that disease or disorder. The polynuclectide sequence is useful as a source of probes and primers, which can be used to screen libraries, isolate clones, and prepare cloning and sequencing templates.
                                                                              178
                                       119
                                                GKESSIENEIAVLRKIKHENIVALEDIYESPNHLYLVWQLVSGGELFDRIVEKGFYTEKD 120
                                                                                      240
                                                                                                                                                                  Novel isolated human kinase polynucleotide that shares structural similarity with animal kinases including calcium/calmodulin-dependent protein kinases and serine/threonine protein kinases, useful in
FRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKD
                                                                                                                              ASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMST
                                                                                                                  ACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEF
                                                                                                                                                         ESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKN
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                                                                                                                                                                                                                                                                                                                      Amino acid sequence of a human kinase polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Friedrich G,
                                                                                                                                                                                                                                                                                                                                        Human; kinase; human disease; human disorder.
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                                                                                                                                                                                                        FAKSKWRQAFNAAAVVHHMRKLHM 322
                                                                                                                                                                                                                                                              AAB84359 standard; Protein; 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-381667/40.
N-PSDB; AAH25118.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              metabolic disorder; immune related disease; neurological disorder; neurodegenerative disorder; inflammatory disorder; infectious disease; reproductive disorder.
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                                                                                                                                                                60 FRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKD 119
                                                                                                                                                                                     120 ASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMST 178
                                                                                                                                                                                                                                                                                                                                                                                                           ESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                1 MGRKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPA 59
                                                                                                       ACGIPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STK; cancer; cardiovascular disease;
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Length
                                        Indels
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                     1.1e - 104
                                        Mismatches
Score 1246;
                     Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Figure 2; 433pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAKSKWRQAFNAAAVVHHMRKLHM
49.68;
                     73.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; protein kinase; PTK;
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                     Similarity
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                                        237;
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Query Match
                       Local
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07-DEC-2000; 2000WO-US33240.
                           N-PSDB; AAC90432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; kinase;
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                                                                                                                                                                                                               Sequence
                                                                                                                                                                                            family.
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prevention, diagnosis and the polypeptides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate kinase expression. For example, they may be used to treat cancers (especially cancers of hematopoietic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), immune related diseases (e.g. rheumatoid arthritis), neurological disorders (e.g. schlacophrenia), neurodegenerative disorders (e.g. parkinson's disease), inflammatory disorders (e.g. infertility).

Parkinson's disease), inflammatory disorders (e.g. infertility).
Additionally, polynucleotides encoding protein kinases may be used as antigens in the production of antibodies against the protein kinase polypeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify modulators of protein kinase expression and activity.
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                                                                                                                                                                                                                                                                                                                                                                                                              239 ESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKN 298
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                               Murine; Dendritic Cell Kinase; MDCK-3; autoimmune disorder; allergy; wound healing; periodontal disease; inflammatory disease; tumour; infection; Ca2+/calmodulin-dependent kinase family.
                                                                                                                                                                                                                                  MGRKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPA
                                                                                                                                                                                                                                                                                                                                                                    ACGIPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEF
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                                                                                                                                                                                        Score 1241; DB 22;
Pred. No. 2.7e-104;
40; Mismatches 46;
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                                                                                                                                                                                         49.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virca GD,
                                                                                                                                                                                                    Similarity
                                                                                                                                                                   357 AA;
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                                                                                                                                                                                                             Matches 236;
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                                                                               Novel murine and human kinase nucleic acids useful for treating inflammations, infections, tumors, allergies, autoimmune diseases, and for stimulating or suppressing immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMST 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGRKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.1%; Score 1233; DB 22; 72.5%; Pred. No. 1.4e-103; Live 40; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a human kinase polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Ala encoded by GCTGGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human disease; human disorder
                                                                                                                                                                                                    Claim 10; Page 92-94; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAKSKWRQAFNAAAVVHHMRKLHM 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 FAKSKWRQAFNATAVVRHMRRLQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 72.55
Matches 235; Conservative
2001-061546/07
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Homo sapiens
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                                                                        Domain
                                                                                                                                                                         Domain
                                                                                                                                                                                                                 Region
   3;
                                                                                                                                                                               The present sequence represents a kinase polypeptide. The kinase polymorlectides and polypeptides are useful in therapeutic, diagnostic and pharmacogenic applications. They are useful for the detection of mutant kinases, or inappropriately expressed kinases for the diagnosis of a disease or disorder. They are useful for screening for drugs (or high throughput screening of combinatorial libraries) effective in the treatment of symptomatic or phenotypic manifestations of that disease or disorder. The polymucleotide sequence is useful as a source of probes and primers, which can be used to screen libraries, isolate clones, and prepare cloning and sequencing templates.
                                                                                                           Novel isolated human kinase polynucleotide that shares structural similarity with animal kinases including calcium/calmodulin-dependent protein kinases and serine/threonine protein kinases, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238
                                                                                                                                                                                                                                                                                                                                                                                                          61 GKESSIENEIAVLRKIKHENIVALEDIYESPNHLYIVMQLVSGGELFDRIVEKGFYTEKD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMST 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKN 298
                                                                                                                                                                                                                                                                                                                                                                                                FRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKD 119
                                                                                                                                                                                                                                                                                                                                                                           MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKATGKLFAVKCIPKKALK 60
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                        MGRKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of a human phosphorylation effector PHSP-25.
                                                   B;
                                                                                                                                                                                                                                                                                                               49.0%; Score 1231.5; DB 22; Length 356; 72.8%; Pred. No. 2e-103; ive 40; Mismatches 45; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphorylation effector; PHSP; proliferative disorder; disorder; neuronal disorder.
                                                  Zambrowicz
                                                  Friedrich G,
                                                  Turner CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY68793 standard; Protein; 389 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAKSKWRQAFNAAAVVHHMRKLHM 322
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                             (LEXI-) LEXICON GENETICS INC.
         99US-0169428
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 72.89
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                 Scoville J,
                                                                              WPI; 2001-381667/40.
N-PSDB; AAH25119.
                                                            Sands AT;
                                                                                                                                                                                                                                                                                             356 AA;
                                                                                                                                         therapeutics
         07-DEC-1999;
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                                                 Donoho G,
                                                            Abuin A,
                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY68793;
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New human phosphorylation effectors useful for the diagnosis, treatment and prevention of proliferative, immune and neuronal disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baughn MR;
H, Azimzai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lal P, Tang YT, Corley NC, Guegler KJ,
Bandman O, Au-Young J, Gorgone GA, Yue
                                                                             'note= "potential phosphorylation site"
                                                                                                                                                                                                        'note= "potential phosphorylation site"
                                      'note= "potential phosphorylation site"
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375
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                                                                                                                                                                                                                                                                                   'note= "potential phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                      172..184
/note= "STK core catalytic motif"
                                                                                                                      'note= "protein kinase catalytic
                                                                                                                                                                                                                                                                                                                            /note= "PTK core domain"
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Location/Qualifiers
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98US-0173482
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99US-0173482
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DAM, Shih LL;
                                                                                                                                                                                                                                                                                                           .52..208
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N-PSDB; AAZ46162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-JAN-1999;
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12-JAN-1999
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Query Match
Best Local
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given in the specification). The sequences were isolated from cDNA libraries prepared from various human tissues. The PHSP proteins are useful for the diagnosis, treatment and prevention of proliferative disorders, immune disorders and neuronal disorders. The PHSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with decreased PHSP expression/activity. PHSP antagonists are useful for treating or preventing disorders associated
                                                                                                                                                                                                                           NEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQ 126
                                                                                                                                                                                                                                                                                                                                                   246 ISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWR 305
                                                                                                                                                Gaps
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                                                                                                                                                                                 220 VAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDENDSKLFEQILKAEYEFDSPYWDD
                                                                                                                                                                                                                                                                                                                                                              280 ISDSAKDFIRNLMEKDPNKRYTCEQAARHPWIAGDTALNKNIHESVSAQIRKNPAKSKWR
                                                                                                                                                                      KKQTINIR--KIFI---FMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPAFRDSSLE
                                                                                                                                                                                                                                                            127 VLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMSTACGTPGY
                                                                                                                                                                                                                                                                                                        186 VAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDD
                                                                                                                                              8;
                                                                                                                        45.6%; Score 1145; DB 21; Length 389; ilarity 71.0%; Pred. No. 1.7e-95; Conservative 39; Mismatches 45; Indels 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat; calmodulin-dependent protein kinase; clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Foye PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calmodulin-dependent protein kinase clone 29.
                                                                            with increased PHSP expression/activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    De Lecea L,
Sutcliffe JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "encoded by TG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW50159 standard; Protein; 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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, Kilduff
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N-PSDB; AAV18867.
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                                                                                                                                    Similarity
                                                                                                     389 AA;
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Gautvik VT,
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Matches
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AAW50159
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251
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                                                                                                                                                                                                                                                                                                                                                                                                                                               132 KYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                               13 KKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPAFRDSSLENEIAV 71
Nucleic acid encoding hypocretin of rat and mouse - useful for diagnosis and treatment of neurological disease, homeostatic dysfunction etc., also sequence for calmodulin kinase-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 AQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAK
                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                              Length 358;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 AVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAP 359
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                   The present sequence is rat calmodulin-dependent protein
                                                                                                                                                                                                                                           Score 1070; DB 19;
Pred. No. 1e-88;
5; Mismatches 74;
                                                                                                                                                                                                                                                                                       55; Mismatches
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                                                                                          English
                                                                                                                                                                                                                                              42.6%;
                                                                                          Disclosure; Fig 6; 111pp;
                                                                                                                                                                                                                                                                                             207; Conservative
                                                                                                                                                                                                                                                                    Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

In (base; 1 to 1126)

National Institutes of Health, Mammalian Gene Collection (MGC)

In (mpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Http://image.llnl.gov

Plate: LLAM12713 row: 1 column: 19

High quality sequence stop: 623.

1. .1126
                                             ALI34342 DKEZP5470

AM016039 UT-H-B10P

AM38137 of2910.1.5

BC086330 ij210-07.9

B184635 603990418

B1667965 603990418

B1667965 603990418

AA51937 EST59855

AQ055651 CTPH-E1-

AQ041427 CTPH-E1-

AQ041427 CTPH-E1-

AQ078706 CTP-HSP-

BC93960 60293912

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AQ078706 CTP-HSP-

AQ078706 CTP-HSP-

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AW252224 UT-R-BUO-

AW25124 UT-R-BUO-

AW25124 UT-R-BUO-

BBR71015 BBR71015

AW25101 UT-W-BH3-

AW421699 UT-R-BH3-

AW42169 UT-R-BH3-

AW42169 UT-R-BH3-

AW42169 UT-R-BH3-

AW42169 UT-R-BH3-

BE59348 263103 MA

AM850410 UT-M-BH3-

BE59348 263103 MA

AM855600 EST367070

AW355600 EST36770

AW355600 EST36770
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5', mRNA sequence.
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AW52224
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BG173948
BF524803
BF524803
AW122501
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AW521699
                      BM921532
BG102407
BG102407
AM16039
AM383872
BO088372
B1834635
B1667965
AA351937
AQ265651
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BG293660
BG293660
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BC934044
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BI821474 603038366
BI824483 603038855
BI084101 602869466
BMB07335 AGENCOURT
BI084897 602869466
                                                     March 14, 2003, 17:23:21 ; Search time 3882 Seconds
(without alignments)
10208.747 Million cell updates/sec
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                                                                                                        Description
                                                                                                                                                                                  32308132
        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                16154066 seqs, 8097743376 residues
                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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31.1
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Minimum DB seq Maximum DB seq

Word size Searched:

Database :

Perfect score: Sequence: Scoring table:

Title:

nucleic

Run on:

787 762 710 684 665

426459

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Score

Result No.

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241 CCTGCCTTCCGGGACAGCCTGGAGAATGAGATTGCTGTGTTGAAAAAGATCAAGCAT 300
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Best Local Similarity 100.
Matches 762; Conservative
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                                                          /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: Not1; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oliqo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."
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                                                                                                                                                                                                               Score 787; DB Pred. No. 0; 0; Mismatches
 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5724450"
/clone=lib="NHH_MGC_125"
/lab_host="DH10B"
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Location, Quantifiers

1. 809

/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ Clone="Itaxon:9606"
/ Clone=TrAAGE:5179336"
/ Clone=TrAAGE:5179336"
/ Index organ: pooled brain, lung, testis; Vector:
/ Tab_nost="DH108"
/ Note: Organ: pooled brain, lung, testis; Vector:
pcWY-SPORT6: Site_1: Not1: Site_2: EccRV (destroyed): RNA
source anonymous pool of 6 male brains, age range 23-27; and almale testis, age 69. Library is
nale lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EccRV site is
destroyed upon cloning). Average insert size 1.9 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen): Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
                                                                                                                                                                              809 bp mRNA linear EST 04-OCT-2001
603038366Fl NIH_MGC_115 Homo sapiens cDNA clone LMAGE:5179336 5',
BI821474
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S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC colone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAMIJ47 row: c column: 17
High quality sequence stop: 808.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI824483 · 740 bp mRNA linear EST 04-OCT-2001 603038855F1 NIH_MGC_115 Homo saplens CDNA clone IMAGE:5179957 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L (Dases 1 to 7, 40)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammallan Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMM1448 row: m column: 14
High quality sequence stop: 709.
Location/Qualifiers
rce
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                            GGCATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCTTTACCTTACCCTGAAGAGAGAAC
                                                                                                                                                                                                                                                                                AAGGCTGTGGATTGCTGGTCCATCGGCGTCATCACCTACATATTGCTCTGTGGATACCCC
CCTGCCTTCCGGGACAGCAGCCTGGAGAATGAGATTGCTGTGTTGAAAAAGATCAAGCAT
                             GAAAACATTGTGACCCTGGAGGACATCTATGAGAGCACCACCCCACTACTACCTGGTCATG
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                                                                                                                                                                                                                                                                                                                          ACTGCCTGTGGGACCCCAGGCTACGTGGCTCCAGAAGTGCTGGCCCAGAAACCCTACAGC
                                                                                      CAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCTGGAGCGGGGTGTCTACACAGAG
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/db_xref="taxon:9666"
/clone="TwAGE:5179957"
/clone=lib="NHH_MGC_115"
/lab_host="DH10B"
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BI824483.1 GI:15936033
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1048 bp mRNA linear EST 20-JUN-2001 Homo sapiens cDNA clone IMAGE:5013856 5',
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male lung, age 27; and 1 male testis, age 69. Library i oligo-dT primed and directionally cloned (Ecorks site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
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Best Local Similarity 100.0%; Pred. No. 2.2e-284;
Matches 710; Conservative 0; Mismatches 0;
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xxef="taxon:9606"
/clone="IMAGE:5013856"
/clone="IMAGE:5013856"
/clone=lib="NIH_MGC_102"
/tissue_type="*epidermoid carcinoma, cell line"
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Directionally cloned into EcoRIX/XhoI sites using the following 5' adaptor: GGGAGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

1 a 298 c 264 g 254 t lothers
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                                                                                    L motional institutes of nearth, mammattain dens collection (mot) Contact: Robert Strausberg, Ph.D.
Email: ogapba: Temail.nih.gov
Elsaue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
CLONE distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://amage.lln.gov
Plate: LLCM1820 row: d column: 17
High quality sequence stop: 853.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1048)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 AAGTGGAGCAGGGCTTAGCAGGAGCAGTTTCTGGCCAGAAGCACCAGCCTGCTGCCAGCG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 GGGCAGCCCCTCATAGGAGGCCCAGGAGGAGCCCCAAGGCGTAGAAGCCTTGTTGAAGC 301
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                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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28.0%; Score 684; DB
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 684; Conservative 0; Mismatches
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AGENCOURT_6575096 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5732298 BM807335
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/db_xref="taxon:9606"
/clone="twa6E:5732298"
/clone_lib="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_hogt="DH108"
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11 MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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CTGGAGGCAATGGGTCGAAAGGAAGAAGATGACTGCAGTTCCTGGAAGAAACAGACCACC 155
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1820 row: d column: 17
High quality sequence stop: 832.
High quality sequence stop: 832.
                                                                              AACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTT
                                 TTCCTGGTGAAGCAAAGACTGAACTGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCA
                                                                                                              CCTGCCTTCCGGGACAGCAGCCTGGAGAATGAGATTGCTGTGTTGAAAAAGATCAAGCAT
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                 /note="Organ: brain; Vector: pCNV-SPORT6; Site_1: Not1; Site_2: ECORV (destroyed); RNA source anonymous pool of 6 male brains, age range 23.27 yo. Library is oligo-dr primed and directionally cloned (Ecorv site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIHMC Library."
                           BI753035 731 bp mRNA linear EST 25-SEP-2001
603025844F1 NIH_MGC_114 Homo sapiens CDNA clone IMAGE:5196323 5',
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100.0%; Pred. No. 1.9e-259;
ive 0; Mismatches 0; Indels (
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http://image.llnl.gov
Plate: LLAMil191 row: g column: 12
High quality sequence stop: 729.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  1. .731
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/db_xref="taxon:9606"
/clone="IMAGE:5196323"
/clone=lib="NHH_MGC_114"
/lab_host="DH10B"
                                                                                 BI753035.1 GI:15744613
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                                                       mRNA sequence.
BI753035
                                                                                                                         Homo sapiens
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RESULT 7
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/note—"Organ: pooled brain, lung, testis; Vector:

pcMv-SPORT6; Site_1: Not1; Site_2: EcoRv (destroyed); RNA
source annonymous pool of 6 male brains, age for 10 male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRv Site is
destroyed upon cloning). Average insert size 1:8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
101. Note: this is a NHH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIB18261 742 bp mRNA linear EST 04-OCT-2001
603032510F1 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5173587 5',
mRNA sequence.
BI818261
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NIH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammallan Gene Collection (MGC)
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1432 row: d column: 04
High quality sequence stop: 742.
                          CTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAATACCTACATGAGAATGGCATCGTCCAC
                                                                                                         AGAGACTTAAAGCCCGAAAACCTGCTTTACCTTACCCTGAAGAAGTCTAAGATCATG
                                                                                                                                                                                                                      553 ATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGGCATCATGTCCACTGCCTGTGGG
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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Pred. No. 1.2e-253;
0; Mismatches 1;
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/clone="IMAGE:5173587"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 812)
NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                      83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-r@mail.nin.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                              TGGAGGACATCTATGAGAGCACCACCACTACTACCTGGTCATGCAGCTTGTTTCTGGTG
                                                                                                                                                                                                                                                                      GCAGGATTCTTCCCGAGTCCCTGGCATCCTCAGAAGCTTCAACTCTGGAGGCAATGGGTC
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                                                  GACTGACTGGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCACCTGCCTTCCGGGACA
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/note—"Organ: pooled lung and spleen; vector: pcWv-SPORT6; Site_1: Not1; Site_2: EcoRv (destroyed); RNA source anonymous pool of 4 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (EcoRv site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NILMGC Library."
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                     20
                       column:
                                                                                                                                                                       /clone="IMAGE:5210299"
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/lab_host="DH10B"
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                                        High quality sequence start: 2
High quality sequence stop: 808
Location/Qualifiers
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http://image.llnl.gov
Plate: LLAM11527 row: m
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/db_xref="taxon:9606"
/clone="InMAGE:5753010"
/clone="InMAGE:5753010"
/clone="InMI-MGC_115"
/lab_host="DH10B"
/clone="Organ: pooled brain, lung, testis; Vector:
pcMv-SpORT6; Site_1: Not!; Site_2: EcoRv (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally cloned (EcoRv site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MC Library."
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                                BM921532 12-MAR-2002 AGENCOURT_6708041 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5753010
                                                                                                                                                                                                                                                                                                                     Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.lln.gov
Plate: LLAM12788 row: b column: 19
High quality sequence stop: 592.
Location/Qualifiers
rce
                                                                                                                                                                      Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1068)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CTGGAGGCAATGGGTCGAAAGGAAGAAGATGACTGCAGTTCCTGGAAGAAACAGACCACC 120
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                                                                         5', mRNA sequence.
BM921532
BM921532.1 GI:19371911
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AUTHORS
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JOURNAL
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RESULT 10
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E Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (Dases 1 to 479)

S Helton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Leenish, J., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hiller, L., Marra, M., Brestelli, J., Gradwohl, G., Clifton, S., Hiller, L., Marra, M., Pape, D., Wylie, T., Marrin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsägareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.

Endocrine Pancreas Consortium

L Unpublished (2000)

Other_ESTS: ij2lo7, yl
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium

Endocrine Pancreas Consortium
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1j21c07.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
EQ102407.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center This clone is
available royalty-free through LLNL; please contact the IMAGE
consortium (info@image.llnl.gov) for further information
Seq primer: -40UP from Gibco
High quality sequence stop: 448.

Location/Qualifiers
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/organ.sm="Homo sapiens"
/db_xref="taxon:9606"
/db_braf="taxon:9606"
/clone="lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
                                                                                                                                                                                                                                                                540
                                                                                                                                                       421 AAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAATACCTACATGAGAAT 480
                                                                             314 GAAAACATTGTGACCCTGGAGGACATCTATGAGGACCACCACCACTACTACTGGTCATG
                                                 CAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCTGGAGCGGGGTGTCTACACAGAG
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/dev_stage="Adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 617-495-8557
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AUTHORS
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fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms POR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                          2200 TAAGGGCTGCAAGGAATTCTTATCCTGGCCACATGTCCTCCGTGCACACACCCAATGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Emall: ggapbs remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI),
Toshiyuki and Piero Carninci (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
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                                                                                                                                                                                                                            Length 479;
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100.0%; Pred. No. 2.5e-188;
iive 0; Mismatches 0;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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BG715920
BG715920.1 GI:
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pBluescript KS+); Site_I: BamHI; Site_E: Sall-MDI (gtcgag pluescript KS+); Site_I: BamHI; Site_E: Sall-MDI (gtcgag size-selected for average insert Size 2: 3kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCATGGAGCGGGGTGTCTACACAGAG 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
                                                                                                                                                                                                        /note="Organ: brain; Vector: pBluescriptR (modified
   can
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Plate: LLAM10688 row: e column: 17
High quality sequence stop: 766.
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                                                                                                                                                                                                                                                                                                                                                                                            Score 473; DB 12;
Pred. No. 6.6e-186;
0; Mismatches 3;
                                                                                                                                                                         /tissue_type="hypothalamus"
/lab_host="DH10B"
                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4799224"
/clone_lib="NIH_MGC_96"
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|larity 99.5%;
|Conservative
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Matches 623
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemannédkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                            Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and Wiemann
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 501)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     German Genome Project.
sl sequence also available.
flus clone (DKFZp5470044) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1585 CAGAGGGAGGAAGGCAGAGCAAGTGGAGCAGGGCTTAGCAGGAGCAGTTTCTGGCCAGAA 1644
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              AL134342

DKFZp5470044_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone
DKFZp5470044 5', mRNA sequence.
                                                                                                                                                                                                                                                                        ,S.
EST (Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B.
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109 t
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/db_xref="taxon.9606"
/clone="DKFZp5470044"
/clone_lib="547 (synonym: hfbrl)"
/tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 450; DB 9; I
Pred. No. 2.8e-176;
0; Mismatches 1;
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154 c 132 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="fetal"
/lab_host="X1-2blue"
                                                                                                  AL134342.1 GI:6602529
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99.8%;
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                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
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                                                                              ACCESSION
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KEYWORDS
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AL134342
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1...46 / Corganism="Homo sapiens"  
// Ab_xref="taxon:9606"  
// Ab_xref="taxon:9606"  
// Ab_xref="taxon:9606"  
// Ab_xref="taxon:9606"  
// Ab_xref="taxon:9606"  
// Ab_xref="taxon:1445"  
// Ab_host="Delio (Life Technologies)"  
// Ab_host="Delio (Life (Life Te
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tunor Gene Index
Unpublished (1997)

Unpublished (1997)

Email: cgapbsrtStrausberg, Ph.D.

Email: cgapbsrtGmail.nih.gov

The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:

NCI-CGAP Clone distribution information can be found through the www-bio.lln.gov/Dbrp/Image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW016039 484 bp mRNA linear EST 10-SEP-1999 UI-H-BIOp-abf-c-11-0-UI.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711445 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 484)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
GTGTCACCTTCTCCAAGCAAAGCCATATGGAGCATCTACCCAGACTCCCACTCTGCACAC 1944
                               ACTCACTCCCACCTCTCAAGCCTCCAACCTCTTGGCCAGATTGGGCTCATTAATGTCGTT
                                                                                                                                                                                     421 ACTCACCTCCACCTCTCAAGCCTCCAACCTCTTGGCCAGATTGGGCTCATAATGTCGTT
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TITLE
1885
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KEYWORDS
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NCI_CGAP_CO10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE CloneIDS 1057416-1061255, 1144584-1145351) The resulting subtracted library contained 4 million recombinants.
Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Racilitate Gene Discovery. Genome Research 6, 791-806.
TAG_LIB=NCI_CGAP_Brn26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA838372 410 bp mRNA linear EST 09-JUN-1998 of29all.sl NCI_CGAP_Kid6 Homo sapiens CDNA clone IMAGE:1422524,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bummalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 410)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
Emmert.Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
                                                                                                                                                                                                                                                                      Length 484;
                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                      17.4%; Score 426; DB 10; I 100.0%; Pred. No. 2.6e-166;
                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                              119
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                           142 g
                                                                                                                                                                                        TAG_SEQ=ATAGG'
89 c
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                                                                                                                                                                                                                                                                                              al Similarity 100.
426; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
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SOURCE
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Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Stratagene, Inc. cDNA Library Preparation: Stratagene, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 944 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="kidney tumor"
/lab_host="SOLR (kanamycin resistant)"
/note="Yorgan: kidney; Vector: Bluescript SK-; Site_1:
/note="Yorgan: kidney; Vector: Bluescript SK-; Site_1:
Oligo dr. Pooled kidney tumors. 5' adaptor sequence: 5'
GAATTGGCACGAG 3' 3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb.
19 c 130 g 89 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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100.0%; Pred. No. 1.2e-159;
tive 0; Mismatches 0;
                                                              www-bio.lln1.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1422524"
/clone_lib="NCI_CGAP_Kid6"
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Fatent No. 6222029
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Lacroix, Aymeric
APPLICANT: Lacroix, Buno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
US-09-247-155-72
PCT-US94-10080-1
US-08-128-738-1
US-09-328-256-13
US-09-395-115-13
US-09-395-115-13
US-09-45-26-13
US-08-43-475-13
US-08-41-794-13
US-08-128-7358-3
US-08-915-755-1
US-08-913-795-1
US-08-915-795-1
US-08-910-785-5
US-08-940-0868-55
US-08-940-0358-55
US-08-940-0358-55
US-08-940-0358-55
US-08-940-0358-55
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| LOCATION: 87..191
| IDENTIFICATION METHOD: Von Heijne matrix
| OTHER INFORMATION: score 5.6
| OTHER INFORMATION: seq FIFMEVLGSGAFS/EV
| US-08-905-223-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: ISraelsen, Ned A.
REGISTRATION UNDRER: 29,655
REFERENCE/DOCKET UNMER:
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo Sapiens
TISSUE TYPE: Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
       STATE: California
COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 536
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Sequence 8, Appli
Sequence 1, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 58, Appli
Sequence 2, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 3, Appli
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Sequence 16, Appli
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                                                                                                                                                                                                  (without alignments) 7736.475 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
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                                                                                                                                                                      March 14, 2003, 17:25:25; Search time 97 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-051-239A-1
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                                                                                                                             nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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length: 200000000
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2447
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Maximum DB seq
                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Word size :
                                                                                                                             OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                        Run on:
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CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/737,980

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: KR 1995-6266

FILING DATE: 24-MAR-1995

INFORMATION FOR SEQ 1D NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 755 Dase pairs

LENGTH: 755 Dase pairs

TYPE: nucleic acid

STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3380;
                                                  0.9%; Score 23; DB 1; Length 296; 100.0%; Pred. No. 0.23; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                               APPLICANT: COWSET, Lex M.
TITLE OF INVENTION: AATISENSE MODULATION OF FAN EXPRESSION
TITLE OF THE REPERBINE: RTS-0009
CURRENT APPLICATION MATER: US/09/156,425B
CURRENT FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
DEVELOPMENTAL STAGE: Fetus at 22 weeks gestation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
TITLE OF INVENTION: Apoptosis Regulating Gene
NUMBER OF SEQUENCES:
OMORPTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.9%; Score 23; DB 2;
100.0%; Pred. No. 0.23;
Live 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                            RESULT 3
US-09-156-425-1
Sequence 1, Application US/09156425B
Patent No. 5862671
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2425 ATATTTTCTCTAAAAAAAAA 2447
                                                                                                                                2425 ATATTTTCTCTAAAAAAAAA 2447
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                                                                                                                                                  Query Match 0.99
Best Local Similarity 100.0
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.9°
Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-156-425-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
CDNA
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; MOLECULE TYPE:
US-08-738-367-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 3380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-08-737-980-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1
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                                                                                                                                                                                           CCTGCCTTCCGGGACAGCAGCCTGGAGAATGAGATTGCTGTGTGTTGAAAAAGATCAAGCAT 300
                                                                                                                                                                                                                                                121 AACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTT 180
                                                                                           1 TGGAGTGGGAGCTCAAGCAGGATTCTTCCCGAGTCCCTGGCATCCTCAGAAGCTTCAACT 60
                                                         Gaps
                                                                                                                                  18 TGGAGTGGGAGCTCAAGCAGGATTCTTCCCGAGTCCCTGGCATCCTCAGAAGCTTCAACT 77
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APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: LaValie, Edward
APPLICANT: Racie, Lisa
APPLICANT: Racie, Lisa
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROFEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                    Length 362;
                Score 287; DB 4; Length 36;
Pred. No. 1.7e-127;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 GAAAACATTGTGACCCTGGAGGACATCTATGAGAGCAC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATORNEY AGENT INFORMATION:
NAME: Brown, Scott A.
REGIESTATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 base pairs
TYPE: nucleic acid
STRANDEDNESS: duuble
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08738367
Patent No. 5827688
                Query Match 11.7%;
Best Local Similarity 99.7%;
Matches 337; Conservative
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CLASSIFICATION: 514
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US-08-738-367-8
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100.0%; Pred. No. 2.1;
            Indels
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                                                                                                                                                                                                               APPLICANT: Bandman, Olga
APPLICANT: Bandman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Guegler, Karl G.
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                 Sequence 12, Application US/09272796
Patent No. 6207148
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pre
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; Patent No. 5750367
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                                            411 CTACACAGAGGATGCCAG 431
                                                                411 CTACACAGAGAAGGATGCCAG 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1282 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
         21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; IMMEDIATE SOURCE:
; LIBRARY: PROSNOTO6
; CLONE: 827431
US-09-272-796-12
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Best Local Similarity
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                                                                                                                              RESULT 6
US-09-272-796-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY:
STATE:
           Matches
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                                                                                                                                                          0.9%; Score 22; DB 2; Length 755; 100.0%; Pred. No. 0.68; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lal, Preeti
APPLICANT: Goll, Surya K.
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
CORRESPONDENCE: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.9%; Score 21; DB 2; 100.0%; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER FADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: TEM COMPATIBLE
COMPUTER: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STAFE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: B1111ngs, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-845-4166
TELEX:
                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/08878989
Patent No. 5885803
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
                                                                                                                                                                                                                              2426 TATTTTCTCTAAAAAAAAA 2447
                                                                                                                                                                                                                                                  726 TATTTTTCTCTAAAAAAAAA 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1282 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                        polyA_signal 713..718
                                                                                                                                                                            Best_Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
TISSUE TYPE: Liver FEATURE: NAME/KEY: CDS
                                    CDS
35..559
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Best Local Similarity
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; CLONE: 827431
US-08-878-989-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                   COCATION:
FEATURE:
NAME/KEY:
LOCATION:
US-08-737-980-1
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OFFRAING STSIEM: PC-10.2/MS-LOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,647B
FILING DATE: 02-JUN-1995
CLASSIFICATION NUMBER: US/08/456,647B
FILING DATE: 02-JUN-1995
PRIOR APPLICATION NUMBER: US 08/237,401
FILING DATE: 02-MAY-1994
PRIOR APPLICATION NUMBER: US 07/884,486
FILING APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07251/007002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-084.456-647B-5/C
Sequence 5, Application US/08456647B
Sequence 5, Application US/08456647B
GENERAL NO. 5811516
GENERAL INFORMATION:
APPLICANT: Lemke Ph.D. et al., Greg E.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                    FILING DATE: may ..., ...
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/149,103
FILING DATE: NO. 5798209ember 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Knight, Matthew W.
REGISTRATION NUMBER: 36,846
REFERENCE/DOCKET NUMBER: 31,2468
REFERENCE/DOCKET NUMBER: 31,246
REFERENCE/DOCKET NUMBER: 36,846
REFERENCE/DOCKET NUMBER: 36,846
FELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELEPX: 67-3510
STOWNMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20; DB 1;
Pred. No. 6.2;
OPERATING SYSTEM: IBM MS-DOS (Version 6.22) SOFTWARE: WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALUNESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUMPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                              US/08/451,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1309 GGGCCCTGTGGCTGCTC 1328
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100.0%;
                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: May 26, 1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 3116 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.8%
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear US-08-451-883-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
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Sequence 2, Application US/08451883

Sequence 2, Application US/08451883

Patent No. 5798209

GENERAL INFORMATION:

APPLICANT: Lawrence C.B. Chan

TITLE OF INVENTION: HUMAN AND MOUSE VERY LOW DENSITY

TITLE OF INVENTION: LIPOPROTEIN RECEPTORS

TITLE OF INVENTION: USE OF SUCH RECEPTORS

NUMBER OF SEQUENCES: 4

NUMBER OF SEQUENCES: 4

ADDRESSEE: LYON & LYON

STREET: 633 West Fifth Street, Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 3116; 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                           APPLICAMY: LAMPERGE C. B. CHAN
TITLE OF INVENTION: HUMAN AND MOUSE VERY LOW
TITLE OF INVENTION: DENSITY LIPOPROTEIN RECEPTORS
TITLE OF INVENTION: AND METHODS FOR USE OF SUCH
TITLE OF INVENTION: RECEPTORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 611 West Sixth Street
CITY: Los Angeles
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURKENT APPLICATION DATA:
CURKENT APPLICATION DATA:
FILING DATE:
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
TELING DATE:
APPLICATION NUMBER:
TILING DATE:
APPLICATION NUMBER:
ATTORNEY AGENT INFORMATION:
NAME:
REFERENCE/DCCKET NUMBER:: 204/052
REGISTRATION NUMBER:: 204/052
REGISTRATION NUMBER:: 204/052
TELECHHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELERATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3116 base pairs
TYRANDENNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 633 West Fifth Street, Suite 4700 CITY: Los Angeles STATE: California CUMYRY: U.S.A. ZIP: 90071-2066 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 20;
Pred. No.
                                   Lawrence C. B. Chan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.8%; Sc
Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
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US-08-149-103-2
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Gaps

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100.0%; Pred. No. 6.2;
           Indels
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                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie R.
APPLICANT: Scadden, David T.
APPLICANT: Baker, Kevin P.
TITLE OF INVENTION: Protein Tyrosine Kinases
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Preu. ...
           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Datin (Geneticch)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/445,640
FILING DATE: 22-MAX-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/17058
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: 08/157563
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: HASAK, JANGE E.
REGISTRATION NUMBER: 28,616
                                                                                                                                                                                                                                                                                                                                                      STREET: 460 Point San Bruno Blvd CITY: South San Francisco STATE: California
                                                                                                                                                          US-08-445-640-9/c
; Sequence 9, Application US/08445640
; Patent No. 5709858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08170558; Patent NO. 6001621
GENERAL INFORMATION: APPLICANT: GOOWSKI, Paul J. APPLICANT: Mark, Melanie R.
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                                               1317 TGGCTGCTCCTGCTGCC 1336
                                                                     2789 IGGCIGCICCAGCIGCC 2770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2632 TGGCTGCTCCTCCAGCTGCC 2613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1317 TGGCTGCTGCTCCAGCTGCC 1336
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Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415/952-9881
TELEX: 910/71-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94080
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US-08-170-558-9/C
       20;
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         Matches
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O.8%; Score 20; DB 1; Length 3307;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 20; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 02-MAX-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05/084/486
FILING APPLICATION DATA:
APPLICATION NUMBER: 05 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Haile Ph.D., 11sa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07251/007001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LANGER Ph.D. et al., Greg E.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 5, Application US/08237401A

; Patent No. 5837448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3307 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.8%; S
100.0%;
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3307 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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237..2859
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237..2859
                                                                                       TOPOLOGY: Linear
MOLECULE TYPE: DNA
IMMEDIATE SOURCE:
CLONE: TYTO-3
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
CLONE: Tyro-3
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92037
                                                                                                                                                                                                             ; LOCATION:
US-08-456-6478-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY:
; LOCATION:
US-08-237-401A-5
                                                                                                                                                                                            NAME/KEY:
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22-MAY-1995

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Patent No. 6096527
GENERAL INFORMATION:
APPLICANT: Goddwski, Paul J.
APPLICANT: Bark, Melanie R.
APPLICANT: Backer, Kevin P.
APPLICANT: Barch, Will F.
TITLE OF INVEWTION: Protein Tyrosine Kinases
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STRATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
COFFWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 22-MAY-1995
CLASSIFICATION: 530
LOR APPLIANCE
                                                                                                                                                                                                                                                                                                               854C1D2
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APPLICATION NUMBER: 08/170558
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/157563
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION NAMER: 08/170558
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/157563
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    854C3
                                                                                                                                                                                                                                                             NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REGISTRATION NUMBER: 854C1
TELECOMMUNICATION INFORMATION:
TELEPAN: 415/225-1891
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3778 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 85.4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1317 IGGCIGCTGCTCCAGCIGCC 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2632 TGGCTGCTCCAGCTGCC 2613
                                                                                                                                                                                                                                                                                                                                                                                                                                                              : STRANDENESS: single
: TOPOLOGY: linear
US-08-447-314-9
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US-08-445-461-9/c
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APPLICANT: Scadden, David T.
APPLICANT: Baker, Kevin P.
APPLICANT: Baron, Will F.
TITLE OF INVENTION: Protein Tyrosine Kinases
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
ZIP: 94080
CONNTRY: USA
                                                                                                                                                                                                                                                                                                               ZIP: 940BU
COMPUTER: 5.25 inch, 360 Kb floppy disk MEDDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,558
FILING DATE: 20-DEC-1993
CLASSIFICATION: 435
FILING DATE: 20-DEC-1993
ATTORNEY APPLICATION: 435
PRIOR APPLICATION NUMBER: 08/157563
FILING DATE: 23-NOV-1993
ATTORNEY AGENT INPORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKT NUMBER: 854C1
TELEPHONE: 415/25-1896
TELEEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
WYDE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-08-447-314-9/C
Sequence 9, Application US/08447314
Fatent No. 6087144
GENERAL INFORMATION:
APPLICANT: Scadden, David T.
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
TITLE OF INVENTION: Protein Tyrosine Kinases
NUMBER OF SEQUENCES: 35
CORRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: patin (Genentech)
APPLICATION NUMBER: US/08/447,314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2632 TGGCTGCTGCTCCAGCTGCC 2613
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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US-08-170-558-9
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                                                                                                                                                                                                                                                                                                                                                               0.8%; Score 20; DB 3; Length 3785; 100.0%; Pred. No. 6.2; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15

UGS-08-466-120-1

Sequence 1, Application US/08466120

Sequence 1, Application US/08466120

Patent No. 5869284

GENERAL INFORMATION:

APPLICANT: CAO, ET AL.

TITLE OF INVENTION: Retinoic Acid Receptor Epsilon NUMBER OF SEQUENCES: 4

CORRESPONDENCES: 4

CORRESPONDENCES: 4

CORRESPONDENCES: 4

CORRESPONDENCES: 4

CORRESPONDENCES: ABENER OF SEGRET OF STEWNE, BAIN, GILFILLAN, STRET: GEGENT OF SEGRET OF STEWNE, BAIN, GILFILLAN, STRET: GEGENT OF SEGRET OF SEGRET OF STEWNE, BAIN, GILFILLAN, STRET: GEGENT OF SEGRET OF STEWNE, BAIN, GILFILLAN, STRET: USA JENEY OF SEGRET OF STEWNE, BAIN, GILFILLAN, STRET: USA JENEY OF STEWNE, BAIN, GILFILLAN, STRET: USA JENEY OF STEWNE, WAS-DOS OFFWATER: USA STEWNE, STEWNE, WAS-DOS OFFWATER: WORD PERFECT 5.1

CURRENT APPLICATION NUMBER: US/08/466,120

FILING DATE: 24 JUN 94

ATTORNAY/AGENT INFORMATION:

NAME: FERRANCE/DOCKET NUMBER: 35,134

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 35,134

REFERENCE/DOCKET NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 37,134

REFEREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1317 TGGCTGCTGCTCCAGCTGCC 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 2632 TGGCTGCTCCAGCTGCC 2613
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; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 9;
SEQUENCE CHARACTERISTICS:
; LENGTH: 3785 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLGX: linear
US-08-445-461-9
                                                                                                                                                                                                                                                                                                                                                        Query Match 0.8°
Best Local Similarity 100°
Matches 20; Conservative
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MOLECULE TYPE: CDNA
US-08-466-120-1
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Search completed: March 15, 2003, 05:02:39

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

March 14, 2003, 14:08:41; Search time 16 Seconds (without alignments) 1371.239 Million cell updates/sec Run on:

US-09-960-643-2 Perfect score: Title:

1 MGRKEEDDCSSWKKQTTNIR.....VKASGSSHCRAGQTGVCLIM 476 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

199416 seqs, 46092074 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries

Database

Published_Applications_AA:*

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11: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	i and a openions	Segmence 3 Appli			. 4			6 Seguence 16.	Sequence 2. A	Sequence 2.	Sequence 4. A	Sequence 4.	Sequence 2. 7	-	Sequence 2. Appli	Segmence 2. Appli	Sequence 6. Appli	٠,	ͺ ⋖
SUMMARIES			ΠD	US-09-935-464-5	US-09-935-464-3	US-10-024-036B-2	US-10-142-356-7	US-09-817-181-4	US-09-935-464-36	US-09-817-181-2	US-09-835-788A-16	US-09-797-039-2	US-10-153-921-2	US-10-217-357-4	US-09-975-326-4	US-09-934-406-2	US-10-217-357-2	US-09-975-326-2	US-10-116-332-2	US-10-142-356-6	US-10-096-960-4	US-10-024-036B-5
			DB	6	0	6	σ	10	σ	10	10	10	12	σ	10	σ	σ	10	σ	σ	12	6
		Query	Length	476	460	357	370	370	317	326	280	501	501	765	765	166	166	166	385	545	556	648
	dР	Query	Match	100.0	94.0	49.6	45.9	45.9	45.8	40.4	37.6	29.7	29.7	24.9	24.9	24.9	24.9	24.9	24.1	23.7	23.6	23.3
			Score	2513	2362	1246	1152.5	1152.5	1151	1016.5	944.5	747.5	747.5	625.5	625.5	625.5	625.5	625.5	606.5	594.5	592	585.5
		Result	No.	П	7	e	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19

Sequence 4, Appli Sequence 1, Appli	Sequence 2, Appli	Sequence 23, Appl	Sequence 16, Appl	Sequence 11, Appl		Sequence 17, Appl		Sequence 2, Appli	Sequence 238, App	Sequence 17, Appl	Sequence 265, App	Sequence 266, App	Sequence 814, App	Sequence 38, Appl	Sequence 39, Appl	Sequence 210, App	Sequence 18, Appl	4	Sequence 18, Appl	~	Sequence 22, Appl	Sequence 19, Appl	Sequence 188, App	Sequence 9, Appli
US-09-992-481-4 US-09-740-627-1	US-10-096-960-2	US-09-988-462-23	US-10-081-119-16	US-09-740-627-11	US-09-988-462-25	US-09-854-731-17	US-09-922-138-5	US-09-841-683-2	US-09-771-161A-238	US-09-858-664A-17	US-09-771-161A-265	US-09-771-161A-266	US-09-764-868-814	US-09-828-313-38	US-09-828-313-39	US-09-771-161A-210	US-09-858-664A-18	US-10-081-119-34	US-09-854-731-18	US-09-854-731-4	US-09-988-462-22	US-09-854-731-19	US-09-771-161A-188	US-09-740-627-9
10	12	σ	0	10	σ	10	10	10	10	10	10	10	6	10	10	10	10			10	σ	10	10	10
817 543	265	295	821	522	463	639	514	514	454	298	740	740	265	597	549	406	508	370	625	623	464	576	387	459
23.3	22.7	22.4	22.2	22.1	21.6	21.4	21.1	21.1	21.1	20.5	20.4	20.4	20.3	20.3	20.1	20.1	20.0	19.8	19.8	19.7	19.5	19.3	19.2	19.1
585.5 575.5	571.5	563.5	558	556.5	542.5	538.5	531	531	530	514	513	513	508.5	508.5	206	505.5	502.5	498	496.5	495.5	490	486	483	480.5
20	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: Meyer, Joanne
APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martington-Martingt
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100.0%; Pred. No. 1.3e-181;
iive 0; Mismatches 0;
US-09-935-464-5; Application US/09935464; Sequence 5; Application US/09935464; Publication No. US20030027153A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 100.
Matches 476; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-464-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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61 GKESSIENEIAVLRKIKHENIVALEDIYESPNHLYLVMQLVSGGELFDRIVEKGFYTEKD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 1246; DB 9; Length 357;
; Pred. No. 2.6e-86;
40; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/10142356
Sequence 7, Application US/10142356
Publication No. US20030036183A1
GENERAL INFORMATION:
APPLICANT: BOWERS, Alex J.
TITLE OF INVENTION: Serine-Threonine Kinase Member, h2520-40
FILE REFERENCE: 01017/3117A
CURRENT APPLICATION NUMBER: 2002-05-09
PRIOR APPLICATION NUMBER: 60/290,276
PRIOR PLINE DATE: 2001-05-10
NUMBER: OF THE CONTROL OF THE CONTR
                                                                                                                                                                                                                                               TITLE OF INVENTION: 68730 and 69112, Protein Kinase TITLE OF INVENTION: 68730 and 69112, Protein Kinase TITLE OF INVENTION: MOLECULES and USES Therefor FILE REFERENCE: MPI2000-521P1R(M) CURRENT APPLICATION NUMBER: US/10/024,036B CURRENT FILING DATE: 2001-12-17 PRIOR FILING DATE: 2000-12-22 NUMBER OF SEQ ID NOS: 10 SOFTWARE: FastSEQ for Windows Version 4.0
                           SCENIGSKGKSSYCSEPTLLKKANKKQ 447
                                                                                                                                                                        ; Sequence 2, Application US/10024036B
; Publication No. US20030028004A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAKSKWRQAFNAAAVVHHMRKLHM 322
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Best Local Similarity 73.1%;
Matches 237; Conservative 40
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SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-024-036B-2
                                                                                                                             RESULT 3
US-10-024-036B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2
LENGTH: 357
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SEQ ID NO 7
421
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US-09-935-464-3
US-09-935-464-3
Sequence 3, Application US/09935464
Publication No. US20030027153A1
GENERAL INFORMATION:
APPLICANT: Meyer, Joanne
APPLICANT: Meyer, Joanne
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/1H702 US1
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT PILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-01-09
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100.0%; Pred. No. 3e-170;
Live 0; Mismatches 0;
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
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Best Local Similarity 100.
Matches 447; Conservative
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ORGANISM: Homo sapiens
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 36
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                                                                                                                                                                 AVVHHMRKLHMNLHSPG 328
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Matches 220; Conservative
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Sequence 4, Application US/09817181

Sequence 4, Application US/09817181

GENERAL INCORDATION:

APPLICANT: MERKULOV, Gennady et al

APPLICANT: MERKULOV, Gennady et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/817,181

CURRENT APPLICATION NUMBER: US/09/817,181

CURRENT FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 4
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                                         DB 9;
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Pred. No. 3e-79;
                                       45.9%; Score 1152.5; Di 55.8%; Pred. No. 3e-79;
                                                                  46; Mismatches
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  Homo sapiens
                                                  Best_Local Similarity
Matches 239; Conserv
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ORGANISM: Human
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; ORGANISM: H
US-10-142-356-7
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                                       Query Match
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APPLICANT: Meyer, Joanne
APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TILLANT: PARKER, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSY
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REPERENCE: 3322/1H702 US1
CURRENT APPLICATION NUMBER: US/09/935,464
PRIOR PILING DATE: 2001-08-23
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09 5 251 AKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFN 309 310 AAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAPVLDHSVALPA 369 370 LTQLPCQHGRRPTAPGGRSLNCLVNGSLHISSSLVPMHQGSLAAGPCGCCSSCLNIGSKG 429 73 KKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVK 132 133 YLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMSTACGTPGYVAPEVL 191 Gaps 190 VLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISES 14 KOTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPAFRDSSLENEIAVL AQKPYSKAVDCWSIGV1TY1LLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAK Length 317 ; Score 1151; DB 9; ; Pred. No. 3.2e-79; 44; Mismatches 51;

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70 AVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLS 129
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Sequence 2, Application US/09797039

Patent No. US20020042099A1

GENERAL INFORMATION:

APPLICANT: Olandt, Peter J

APPLICANT: Rapeller Libermann, Rosana

TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN

TITLE OF INVENTION: KINASE FAMILY MEMBERS AND USES THEREFOR

TITLE OF INVENTION: LA48-017001

CURRENT APPLICATION NUMBER: US/09/797,039

CURRENT FILING DATE: 2001-02-28

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSEO for wills.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
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                                                                                                                                                                Query Match 37.6%; Score 944.5; DB 10
Best Local Similarity 77.5%; Pred. No. 9.7e-64;
Matches 176; Conservative 26; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 29.7%; Score 747.5; DB 1 Similarity 35.9%; Pred. No. 1.5e-48;
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                     ORGANISM: Homo sapiens
                                                                                                                           US-09-835-788A-16
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LENGTH: 501
TYPE: PRT
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                                       SEQ ID NO 16
LENGTH: 280
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US-09-797-039-2
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Best Local 8
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APPLICANT: Ni et al.

ITILE OF INVENTION: Death Domain-Containing Receptor Polynucleotides, Polypeptides,

ITILE OF INVENTION: Antibodies

FILE REFERENCE: PT018P1

CURRENT APPLICATION NUMBER: US/09/835,788A

CURRENT FILING DATE: 2001-04-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 1999-10-18

PRIOR FILING DATE: 1999-10-18

PRIOR FILING DATE: 1999-10-18

PRIOR FILING DATE: 1999-11-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 ASLVIQOVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMST 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEF 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAKSKWRQAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVLDHSVALPALTQLPCQHGRRPTAPGGRSLNCLVNGSLHISSSLVPMHQGSLAAGPCGC 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 FRD------VLGTIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERD 73
                                                                                              Sequence 2, Application US/09817181
Patent No. US20020142427A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: THEREOF
FILE OF INVENTION: THEREOF
FILE REFERENCE: CL001189
CURRENT PILION DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 40.4%; Score 1016.5; DB 10; Lengt
Best Local Similarity 55.7%; Pred. No. 4.5e-69;
Matches 211; Conservative 34; Mismatches 47; Indels
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Patent No. US20020077458A1
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  301 AVVRHMRKLQLGTSQEG
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TYPE: PRT
ORGANISM: Human
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Sequence 4, Application US/09975326; Patent No. US20020128458A1; GENERAL INFORMATION:
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                                                                                                                                DSTAPEGATG 477
                                                               418 VTPVTDRSATP---
                                                                                                 462 SSHCRAGQTG 471
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US-10-217-357-4
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LENGIH: 765
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Patent No. US20020142430a1

Sequence 2, Application US/10153921

Sequence 2, Application:

Sequence 2, Application:

APPLICANT: YAN, Chunhua et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: UNDER: US/10/153,921

CURRENT FILING DATE: 2002-05-24

PRIOR PRILAGATION NUMBER: 09/734,030

PRIOR FILING DATE: 2000-05-30

PRIOR FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENTH: 501
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251 YWDDISQAAKDLVTRIMEVEQDQRITAEEAISHEWISGNAASDKNIKDGVCAQIEKNFAR 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
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                                                                                                                                                                                       TPATDGSVTPATDRSATPATDGRATPATEESTVPTTQSSAMLATKAAATPEPAMAQPDST 470
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251 YWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWISGNAASDKNIKDGVCAQIEKNFAR 310
                                                                 -----RAPE--QSSTAAAQSASAIDIAIPGA 350
                                                                                                                                  351 AGGATAAAASGATSAPEGDAARAAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSI 410
                                                                                                                                                                  412 AAGPCGCCSSCLN----IGSKGKSSYCSEPTLLKKANKKQNFKSEVMV---PVKASGSSH 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 AVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLS 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 VLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETE-----SKLFEKIKEGYYEFESP
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                               SKWRQAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAPVL
                                                                                                  --- DHSVALPALTQLPCQHGRRP----TAPGGRSLNCLVNGSL--HISSSLVPMHQGSL
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                                                                 311 AKWKKAVRVTTL---MKRL----
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Matches 173; Conservative
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; ORGANISM: HOMO SAPIEN
US-10-153-921-2
                                                                                                                                                                                                                                     465 CRAGQTG 471
                                                                                                                                                                                                                                                                     471 APEGATG 477
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US-10-153-921-2
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Sequence 4, Application US/10217357

Sequence 4, Application US/10217357

Publication No. US20030023063A1

GENERAL INFORMATION:

APPLICANT: Turner, C. Alexander Jr.

APPLICANT: Mathur, Brian

TITLE OF INVENTION: No. US20030023063Alel Human Kinases and Polynucleotides Encod

TITLE OF INVENTION: Same

CURRENT APPLICATION NUMBER: US/10/217,357

CURRENT APPLICATION NUMBER: US/208-09

PRIOR FILING DATE: 2001-10-11

PRIOR FILING DATE: 2000-110-11

PRIOR APPLICATION NUMBER: US 60/239,821

PRIOR APPLICATION NUMBER: US 60/239,821

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASESQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      485 KYTERDGSAMYYNLANALRYLHGLSIVHRDIKPENLLVCEYPDGTKSLKLGDFGLATVVE 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |: ::|||::||:|| | DKAKCCGKEHLIENEVSILRRVKHPNIIMLVEEMETATELFLVWELVKGGDLFDAITSST 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                               L-----AAGPCGCCSSCLNIGSKGKSSYCSEPTLLKKANKKQNFKSEVMV---PVKASG 461
                                                                                                                           ---AIDGRATPATEESTVPTIQSSAMLATKAAATPEPAMAQP 467
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2 GRKEEDDCSSWK----
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US-10-217-357-2
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US-10-217-357-2
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         APPLICANT: Mathur, Brian
TITLE OF INVENTION: No. US20020128458Alel Human Kinases and Polynucleotides Encoding
FILE REFERENCE: LEX-0254-035
CURRENT APPLICATION NUMBER: US/09/975,326
CURRENT FILING DATE: 2001-10-11
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 765
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Fublication No. US20020192204A1
GERREAL INFORMATION:
TITLE OF INVENTION: 15985, A NOVEL HUMAN SERINE/THREONINE
TITLE OF INVENTION: PROTEIN KINASE FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-078001
CURRENT APPLICATION NUMBER: US/09/934,406
CURRENT FILING DATE: 2001-08-21
PRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASTSEQ for Windows Version 4.0
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APPLICANT: Turner, C. Alexander Jr
                                                                                                                                                                                  TYPE: PRT
ORGANISM: homo sapiens
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LENGTH: 766
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APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Brian
TITLE OF INVENTION: No. US20030023063Alel Human Kinases and Polynucleotides Encodi
TITLE OF INVENTION: Same
FILE REFERENCE: LEX-0254-USA
CURRENT PEPLICATION NUMBER: US/09/975,326
PRIOR PELING DATE: 2001-10-11
PRIOR PILING DATE: 2001-10-11
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 766
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RESULT 15
US-09-975-326-2
US-09-975-326-2
Patent No. US20020128458A1
FAPLICANT: US20020128458A1
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVEWTION: No. US20020128458A1el Human Kinases and Polynucleotides Encoding
TITLE OF INVEWTION: No. US20020128458A1el Human Kinases and Polynucleotides Encoding
FILE REFERENCE: LEX-0254-USB
CURRENT APPLICATION NUMBER: US/09/975,326
CURRENT FILING DATE: 2001-10-11
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 766
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366 GGPELDRCISPEGVNGNRCSESSTLLEKYKIGKVIGBGNFAVVKECIDRSTGKEFALKII 425
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Job time : 19 secs
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ORGANISM: homo sapiens
US-09-975-326-2
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                                                                             Human CAMK-X1
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                                                      AAD36148
AAD36155
AAD36157
AAD36158
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AAD36908
AAV04278
AAD00307
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AAX06835
AAS46279
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ABK31158
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ABC88709
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ABC24014
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ABC24015
AAF74277
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AAQ88688
AAV55888
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ABL99884
ABN35390
AAS70157
AAS68767
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AAH13806
                                             AAS90919
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70..1500
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2000US-237419P.
2000US-237423P.
2000US-238558P.
2001US-290555P.
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WO200224947-A2.
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02-OCT-2000; 2
02-OCT-2000; 2
04-OCT-2000; 2
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The invention relates to a method for screening biologically active agent that modulates cancer associated protein kinase function. The invention also relates to a method for diagnosing cancer comprising determining the upregulation of expression of a nucleic acid sequence encoding a protein kinase. The method is useful for diagnosing cancer. A protein kinase is useful for accening biological agents that modulate cancer associated protein kinase function. Downregulating the activity of protein kinase is useful for inhibiting the growth of a cancer cell, e.g. liver or colon useful for inhibiting the growth of a cancer cell, e.g. liver or colon derived tumours and inflammatory samples such as arthritic synovium, for amplified DNA in the cell or increased expression of corresponding mRNA or protein and is also useful to detect differences in expression levels such as molecular weight, amino acid and nuclectide sequences between the located or characterial contracted or characterial contracted or colon corresponding mRNA or protein and is also useful to detect differences in expression levels on the colon characterial contracted or colon and is also useful to detect differences in expression levels and contracted or characterial contracted or colon and is also useful to detect differences in expression levels and contacted or colon and is also useful to detect differences in expression levels to colon and a molecular weight, amino acid and nuclectide sequences between the color or colon and an activity of the colon and an activity and colon and and nuclectide sequences between the color of colons and colo expression ulation of Diagnosing cancer, comprises determining the upregulation of expressiof a nucleic acid sequence encoding a protein kinase or upregulation expression of the protein kinase, in the cancer Claim 16; Page 62-64; 87pp; English. KINETEK PHARM INC. UNIV BRITISH COLUMBIA. Delaney AD; 2002-394145/42. P-PSDB; AAE22764. Yoganathan T, (KINE-) (UYBR-) (

Sequence 2447 BP; 590 A; 707 C; 604 G; 546 T; 0 other;

located on chromosome 1q32.1-32.3

180 240 300 Gaps 9 9 AACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTT 1 TGGAGTGGGAGCTCAAGCAGGATTCTTCCCGAGTCCCTGGCATCCTCAGAAGCTTCAACT TICCTGGTGAAGCAAAGACTGACTGGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCA **AAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAATACCTACATGAGAAT** GGCATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCTTTACCTTACCCTGAAGAAC .; 0 DB 24; Length Indels ö 100.0%; Score 2447; 100.0%; Pred. No. 0; Mismatches ô Matches 2447; Conservative Best Local Similarity Query Match 61 61 121 181 181 241 121 301 361 361 301 421 481 481 421 Op ò 셤 οy g ò Ω οy g ò qq õ g ò g ò

CTTCCAAACCTGGTGTCTATCCGGCAGAGGGAAGGCAGAGCAAGTGGAGCAGGGCTT 1620 AGCAGGAGCAGTTTCTGGCCAGAAGCACCAGCCTGCTGCCAGCGGGGCAGCCCCTCATAG 1680 099 780 900 CCTGAAACTCAAGCCTCAGAAACCTCTAGACCCCAGCTCCCCTGAGATCACCATCACCGAG CCGTTCTATGAAGAAACGGAGTCTAAGCTTTTCGAGAAGATCAAGGAGGGCTACTATGAG CTTGAGAAGGATCCGAACGAGCGGTACACCTGTGAGAAGGCCTTGAGTCATCCCTGGATT AACTTTGCTAAGAGCAAGTGGAGGCAAGCCTTCAACGCAGCAGCTGTGGTGCACCACATG CCTGAAACTCAAGCCTCAGAAACCTCTAGACCCAGCTCCCCTGAGATCACCATCACCGAG TGCTGCTCCAGCTGCCTGAACATTGGGAGCAAAGGAAAGTCCTCCTACTGCTCTGAGCCC ACACTCCTCAAAAAGGCCAACAAAAAACAGAACTTCAAGTCGGAGGTCATGGTACCAGTT TCTAAGATCATGACTCAGACTTTGGTCTGTCCAAGATGGAACAGAATGGCATCATGTCC ACTGCCTGTGGGACCCCAGGCTACGTGGCTCCAGAAGTGCTGGCCCAGAAACCCTACAGC AAGGCTGTGGATTGCTGGTCCATCGGCGTCATCACCTACATATTGCTCTGTGGATACCCC TTTGAGTCTCCATTCTGGGATGACATTTCTGAGTCAGCCAAGGACTTTATTTGCCACTTG AGGAAGCTACACATGAACCTGCACAGCCCGGGCGTCCGCCCAGAGGTGGAGAACAGGCCG GGCCGCCGGCCCACTGCCCCTGGTGGCAGGTCCCTCAACTGCCTGGTCAATGGCTCCCTC TTCCTGGAGCCTGTGCCTATGTCACTGCAATTTTCAGGAGACATATTCAACTCCTCTGCT CTTCCAAACCTGGTGTCTATCCGGCAGAGGAGGAGGAGGAGCAAGTGGAGCAGGGCTT TGCTGCTCCAGCTGCCTGAACATTGGGAGCAAAGGAAAGTCCTCCTACTGCTCTGAGCCC 1081 1321 1021 1021 1141 1261 1381 601 601 661 661 781 841 841 901 961 961 1081 1141 1201 1261 1321 1381 1441 1501 1501 1561 1621 721 721 781 901 1441 1561 1201 a ò QQ ã 음 $Q_{\underline{Y}}$ OD δ Q δy pp οy qq δ QQ ŏ qq δ g QΛ qq ŏ g δy g δy q Qγ QΩ οy qq ŏ g ŏ g δ

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                                    GAGGCCCAGGAGGCAGCCCCAAGGCGTAGAAGCCTTGTTGAAGCTGTGAGCAGGAGAAGC
                                               GGTGCCCACCAGGTCTCCGTGACCTGCCTGCTCTATGCCCCACACCCTACGTG
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzhalmer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinhibin activity, chemotactic/chemokinetic activity, heemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
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Zhang J
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Yang Y,
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system injuries
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Wehrman T, Xu
Goodrich R,
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Wang Z,
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                                                                                                                The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system incuropathy and localised neuropathies and central nervous system glassass, such as Alzhelmer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and constitution.
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leukaemia;
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                                                                     1428 TGGCAGGTCCCTCAACTGCCTGGTCAATGGCTCCCTCCACATCAGCAGCAGCTGGTGGTCC
                                                                                                                                                                 1488 CATGCATCAGGGGTCCCTGGCCGCGGCCCTGTGGCTGCTGCTCCAGCTGCTGAACAT
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                                                                                                                                        CATGCATCAGGGGTCCCTGGCCGCCGGCCCTGTGGCTGCTGCTCCCAGCTGCTGAACAT
                                                                                                                                                                                                                                1344 TGGGAGCAAAGGAAAGTCCTCCTACTGCTCTGAGCCCACACTCCTCAAAAAGGCCAACAA
                                                 TGGCAGGTCCCTCAACTGCCTGGTCAATGGCTCCCTCCACATCAGCAGCAGCCTGGTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human diagnostic and therapeutic polynucleotide (DITHP) #29
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Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC; Chen A, D'Sa SA, Amshey S, Dahl CR, Dam TC, Daniels SE; Dufour GE, Flores V, Fong WT, Greenawalt LB, Hillman JL, Jones AL; Liu TF, Roseberry AM, Rosen BH, Russor FD, Stockdreher TK, Daffo A; Wright RJ, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen W; Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotides encoding diagnostic and therapeutic proteins, e.g. enzymes, hormones and receptors, useful in diagnostics and therapeutics
                                                                     2000US - 0184777 - 2000US - 0184737 - 2000US - 0184813 - 2000US - 0184837 - 2000US - 0184837 - 2000US - 0185216 - 2000US - 020426 - 2000US - 0204815 - 2000US - 0205286 - 2000US - 0205283 - 2000US - 0205286 - 2000US - 0205286 - 2000US - 0205286 - 2000US - 0205286 - 2000US - 0205288 - 2000US - 0205283 - 2000US - 020528 - 2000US
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2000US-0184773.
2000US-0184774.
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the invention relates to polynuclectides (I) encoding diagnostic and theraperic (DTTHP) polypeptides (II), which include e.g. enzymes, and proteins involved in growth and development and receptors. (I) and may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate DITHP expression. For example, (I) and expression by rectifying mutations or deletions in a patient's genome, that affect the activity of the DITHPs, by expression patient's genome, that affect the activity of the DITHPs, by expression in a patient's genome, that affect the activity of the DITHPs, by spression of it. and (II) may be used to treat diseases, for example, cell proliferative proteins or supplementing the patient's own production of them. (I) and (II) may be used to produce the DITHPs, by inserting the nucleic acids in elected and quantitate the presence of similar nucleic acids in a host conduce why also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in the complementary sequences may also be used as antigens in the production of the antibodies against DITHPs and in assays to identify modulators of DITHP antibodies and activity. The anti-DITHP antibodies may also be used as antigens in the production of antibodies may also be used as diagnostic agents for detecting the artibodies may also be used as diagnostic agents for detecting the assay (ELISA)). Ansayogy 6 the represent human diagnostic and assays (ELISA)). Ansayogy for the invention. Claim 1; Page 310-311; 522pp; English.

31.5%; Score 772; DB 22; Length 2689; Sequence 2689 BP; 642 A; 748 C; 678 G; 621 T; 0 other; Query Match

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                             GGCATCCTCAGAAGCTTCAACTCTGGAGGCAATGGGTCGAAAGGAAGAAGAAGATGACTGCAG
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01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
   nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; pastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation, respiratory disorder; renal disorder; kidney failurer; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                     20000US - 0.179065.
20000US - 0.18658.
20000US - 0.18658.
2000US - 0.186135.
2000US - 0.198123.
2000US - 0.219486.
2000US - 0.219486.
2000US - 0.21686.
2000US - 0.21625.
2000US - 0.22526.
2000US - 0.225758.
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2000US-0230437.
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200005-0231242
200005-0231243
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200005-0231414
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200005-0232081
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2000US-0232399.
2000US-0232400.
2000US-0232401.
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                                                                                                                                                                                                                                                                   31 JAN - 2000; 24 - FEB - 2000; 25 - MAR - 2000; 26 - JUL - 2000; 27 - MUG - 2000; 27 - MUG
                                                                                                                                     Homo sapiens
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2000US-0241787. 2000US-0241808. 2000US-0241808. 2000US-024617. 2000US-0246477. 2000US-0246476. 2000US-0246477. 2000US-0246477. 20000S-0246528 20000S-0246632 20000S-024660 20000S-0246610 20000S-0246611 20000S-0249203 20000S-0249208 20000S-0249208

2000US-0249211. 2000US-0249212. 2000US-0249213.

2000US-0249214. 2000US-0249215. 2000US-0249216. 2000US-0249216.

2000US-0249218. 2000US-0249244. 2000US-0249245.

2000US-0249264. 2000US-0249265. 2000US-0249297. 2000US-0249299.

20000S-0249300 2000US-0250160 2000US-0250391 2000US-0251988 2000US-0251479 2000US-0251479 2000US-0251476

2000US-0246524. 2000US-0246525. 2000US-0246526. 2000US-0246526.

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Dy (1), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are disposed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. daysphagia.

2. anglogenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired inmedications, virus (AIDS) and fundi, ocular disorders e.g. dashetes adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituliary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders e.g. nonallergic rhinitis, renal disorders e.g. respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. recute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and center and produce and also be used to aid wound healing and centering respiratory disorders erg. maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The proposed and produced and inchanced and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  increase or decrease storage capabilities, fat content, lipid, protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACATCCGGAAAACCTTCATTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGAGGCAATGGGTCGAAAGGAAGAAGATGACTGCAGTTCCTGGAAGAAACAGACCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGAGTGGGAGCTCAAGCAGGATTCTTCCCGAGTCCCTGGCATCCTCAGAAGCTTCAACT
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ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                   Ruben SM;
2000US-0251869.
2000US-0251989.
2000US-0251990.
2000US-0254097.
                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
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Matches 355; Conservative
                                                                                                                                                                                                                                                                                                                              Rosen CA, Barash SC,
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P-PSDB; AAU87150.
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    08-DEC-2000;
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11-DEC-2000;
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human secreted proteins, and encode the proteins given in AAY1219 to AAY1219, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proliferation/differentiation activity, cell proliferation/differentiation activity, reproductive hormone activity, tissue growth regulating activity, reproductive hormone crivity, tumour inhibition activity or other activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                 forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytckine activity; cell proliferation; differentiation; hammatopolesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CTGGAGGCAATGGGTCGAAAGGAAGAAGATGACTGCAGTTCCTGGAAGAACAGACCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX51787 to AAX52019 represent 5' expressed sequence tags (ESTs) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 IGGAGTGGGAGCTCAAGCAGGATTCTTCCCGAGTCCCTGGCATCCTCAGAAGCTTCAACT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated brain-derived nucleic acids - used to develop products
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                                                                                                                                                                                                  tag; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide into a membrane, or importing a polypeptide into a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which may have cytokine, immune, regulatory, haematopoiesis regulating, anti-inflammatory or tumour inhibition activity
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                                                                                                                                                                                                    Human; secreted protein; EST; expressed sequence
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                                                                                                                                                            Human secreted protein 5' EST SEQ ID NO: 52
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                                        AAX51838 standard; DNA; 362 BP
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                                                                                 AAX51838;
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2000US-0246528.
2000US-0246532.
2000US-0246609.
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2000US-0226681.
2000US-0226868.
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2000US-0229343.
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2000US-0234997.
2000US-0234998.
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2000US-0246474.
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2000US-0234223
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2000US-0236370
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2000US-0239935
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2000US-0241221
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2000US-0227009
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2000US-0231243
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2000US-0236367
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29-SEP-2000;
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12-SEP-2000;
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22-AUG-2000;
22-AUG-2000;
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23-AUG-2000;
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                                                       TTCCTGGTGAAGCAAAGACTGACTGGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCA 240
                                                                                                                            cDNA encoding novel signal transduction pathway protein, Seq ID 189
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The invention relates to novel isolated polypeptides (I), and the invention relates to novel isolated polypeptides (I), and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune confiscions and graft versus host disease, infectious diseases (e.g. rhematois and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and cher blood related disorders (sickle cell anaemia), myeloproliferative disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. dlancher's disease, Parkinson's disease), chromosomal abnormalities (bown syndrome), ischaemic injury (e.g. stroke), renal abnormalities (bown syndrome), ischaemic injury (e.g. stroke), renal alsorders (e.g. globomerulopephitits), cardiovascular disorders (e.g. disorders (e.g. globomerulopephitits), cardiovascular disorders (e.g. dasorders (e.g. globomerulopephitits), cardiovascular disorders (e.g. disorder (inflammatory disorders), liver disorders (cirhosis), as stimulators of B-cell responsiveness to pathogens, activators of the colliferation in pathologies e.g. acquired immune deficiency syndrome (AlbS). AAS26976-AAS27801 represent novel signal transduction cynthemay protein coding sequences and PCR primers of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 189; 880pp; English.
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20000S-0251030.
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20000S-0251479.
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Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiovascular disorder; ischaemia; anglogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy; gene; ss.
                                                                                                          61 CTGGAGGCAATGGGTCGAAAGGAAGATGACTGCAGTTCCTGGAAGAAACAGACCACC 120
                                                                                                                                                                                                                                 Gaps
                                                      1 TGGAGTGGGAGCTCAAGCAGGATTCTTCCCGAGTCCCTGGCATCCTCAGAAGCTTCAACT 60
                                                                    145 TGGAGTGGGAGCTCAAAGCAGGATTCTTCCCGAGTCCCTGGCATCCTCAGAAGCTTCAACT
                                                                                                                         AACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTT
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 Length 476
                           Indels
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11.2%; Score 274; DB 22; I
100.0%; Pred. No. 6.9e-123;
ive 0; Mismatches 0;
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                           Matches 274; Conservative
  Query Match
Best Local Similarity
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Rosen CA, Barash SC, Ruben SM; 2000US-0249209. 2000US-0249210. 2000US-0249211. 2000US-0249244. 2000US-0249245. 2000US-0249264. 2000US-0251856. 2000US-0251868. 2000US-0251869. (HUMA-) HUMAN GENOME SCI INC 2000US-0246613. 2000US-0249207. 2000US-0249208. 2000US-0249217. 2000US-0249218. 2000US-0249265. 2000US-0249297. 2000US-0249300. 2000US-0250160. 05-JAN-2001; 2001US-0259678 2000US-0249299 2000US-0251030 2000US-0249212 2000US-0249213 2000US-0249214 2000US-0249216 2000US-0251988 2000US-0256719 2000US-0251479 WPI; 2001-581633/65. P-PSDB; AAU87467. 08-NOV-2000)
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New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

Claim 1; SEQ ID No 387; 837pp; English.

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. Alzheimer's disease and amplotrophic lateral sclerosis, infections caused by bacteria, viruses amplotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired inmennodeficiency virus (AIDS) and fungi, ocular disorders e.g. depoparation adaction, qastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies,

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respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotraxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,
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                                                                                                                                                                                                                                                                                                 Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases -
                                                                                                                                                               CTGGAGGCAATGGGTCGAAAGAAGAAGATGACTGCAGTTCCTGGAAGAAGAACAGACCACC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    secreted protein; gene therapy; vaccine; treatment; diagnosis;
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                                                                                                      Length 476;
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                                                                                                      11.2%; Score 274; DB 23; L ilarity 100.0%; Pred. No. 6.9e-123; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein cDNA, SEQ ID NO: 177
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06-MAR-2000; 2000US-0187470
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                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                  Local Simines 274;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; seco
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH64901;
                                                                                                         Query Match
                                                                                                                             Matches
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they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased patients of gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression. The sense and antisense nucleic acids may also be their expression. The sense and antisense nucleic acids may also be treasned of similar nucleic acid sequences in samples, and hence to determine which patients may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antisense to acids may in the production of antisonists) of GENSET polypeptide expression and activity. The present sequence is a GENSET nucleic acid of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ss; gene; secretory protein; secretory polynucleotides; SPTM; SPTM-related disease; somatic gene therapy; germline gene therapy; severe combined immunodeficiency; intracellular parasite protection; fungal parasite; protozoan parasite, cell proliferative disorder; cancer; immune disorder; AIDS; neurological disorder; Parkinson's disease; motor neuron disorder; demyelinating disease; multiple sclerosis; meningitis; abscess; prion disease; cerebral palsy; neuroskeletal disorder; peripheral nervous system disorder; dermatomyositis; polymyositis; myopahhy; myasthenia gravis; mental disorder; Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1177 TICTAATCCTGCCTCTGTTCCCTTTTCTCTTGAAAGTCCAGCACCATTCTTGTCC 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2359 TTCCCCAGTTTCCTCGCCCTCCACCCTCCAGCTTCATGCTCAGTGTTGTGCTTAATAAA 2418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1237 TICCCCAGTTTCCTCGCCCTCCACCCCTCCAGGTTCATGCTCATGCTGTTGTGCTTAATAAA 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2299 TTCTAATCCTGCCTCTGTTCCCTTTTCTCTCCTTGAAAGTCCAGCACACCATTCTTGTCC 2358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.1%; Score 149; DB 22;
100.0%; Pred. No. 5.3e-62;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secretory polynucleotide (sptm) 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGGACATATTTTCTCTAAAAAAAAA 2447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
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2000US-229748P.
2000US-229749P.
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2000US-229751P.
2000US-230016P.
2000US-230583P.
2000US-230505P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL99884 standard; cDNA; 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-AUG-2001; 2001WO-US27297
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Matches 149; Conservative
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05-SEP-2000;
05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
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05-SEP-2000;
05-SEP-2000;
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ABL99884
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RESULT 11 ABN35390

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The invention comprises the amino acid and coding sequences of human secretory (SPTM) proteins. The SPTM DNA and amino acid sequences are useful for treating a disease or condition associated with the expression of functional SPTM. The SPTM NAS sequences are useful for somatic or germline gene therapy to correct a genetic deficiency (e.g. severe combined immunodeficiency). The SPTM DNA sequences are also useful in providing protection against intracellular parasites (e.g. fungal parasites and protozoan parasites). The SPTM DNA and protein sequences are also useful for diagnosing cell proliferative disorders, cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune disorders (e.g. AIDS), neurological disorders (e.g. Parkinson's disease), motor neuron disorders, demyelinating diseases (e.g. multiple sclerosis), meningitis, abscesses, prion diseases, cerebral palsy, neuroskeletal disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, myopathy, mysathenia gravis, and mental disorders (e.g. Tourette's syndrome). cDNA sequences ABL99746 - ABL99229
                                                                                                                                                                                                                                                                                                                                                                                                              Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                           Altus CM, Dufour GE, Chalup MS, Hillman JL.
tht RJ, Gietzen D, Liu TF, Yap PE, Dahl CR;
TL, Rohatgi SD, Harris B, Roseberry AM;
David MH, Panzer SR, Flores V, Daffo A;
thang SC, Au AP, Inman RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide sequences encoding human secretory proteins useful for gene therapy of e.g. genetic deficiency disorders, cancers, and diseases caused by intracellular parasites -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TICCTGGTAGAAACAGACCACCACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGG 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 GGCATCCTCAGAAGCTTCAACTCTGGAGGCAATGGGTCGAAAGGAAGAAGATGACTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders (e.g. Tourette's syndrome). cDNA sequences ABL99/represent human secretory polynucleotides of the invention.
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99.4%; Pred. No. 1.5e-41;
ive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                      Stuart J, Lincoln SE, Altus CM, Lundons AL, Yu JY, Wright RO, Gietzen D, Moniyama MG, Bradley DL, Rohateji SD, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 331; 585pp; English.
                                                                                    20000S-230595P.
2000US-230597P.
2000US-230597P.
2000US-230610P.
2000US-230644P.
2000US-230864P.
2000US-230988P.
2000US-230988P.
                                   2000US-230517P.
2000US-230518P.
2000US-230519P.
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2000US-230896P.
2000US-230897P.
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Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                             (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                     07-SEP-2000; 2000US-230951P.
                                                                                                                                                                                                                                                                                                                                         2000US-231832P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-315658/35.
P-PSDB; ABB97887.
06-SEP-2000; 2
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The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or detecting RNA transcripts and splice variants of detecting RNA transcripts and splice variants of transcriptomes. The libraries may also be used as specialised minical renscriptomes. The libraries may also be used as specialised minical particular biological or pathological state, and so allowing the detection of tissue- and pathology specific genes such as those genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABM27253 to ABM59589 represent oligonucleotide sequences from rats, humans and mice, which are used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1526 TGCAATTTTCAGGAGACATATTCAACTCCTCTGCTCTTCCAAACCTGGTGTCTATCCGGC 1585
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                                                                                                                                                           RNA transcript;
                                                                                                                                                         Human; mouse; rat; splice transcript; detection; RNA transc
splice variant; transcriptome; oligonucleotide library; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Faigler S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 60 BP; 13 A; 18 C; 10 G; 19 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mintz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mintz E,
BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      developmental-specific genes
                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-2000; 2000US-221607P.
                                                                                                                                                                                                                                                                                                                                              20-JUL-2001; 2001WO-IB01903
9
                                                                             (first entry)
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ABN35390 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COMP-) COMPUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-257383/30.
                                                                                                                                                                                                                                                              WO200210449-A2.
                                                                                                                                                                                                                         Homo sapiens.
                                                                             15-JUL-2002
                                                                                                                                                                                                                                                                                                       07-FEB-2002.
                                      ABN35390;
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AAS68767 standard; cDNA; 1774 BP.
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AAS68767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical insolvers involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and advanced to the contract of the polyperial context types of data and products dependent on DNA and advanced to the contract of the polyperial context types of the context procession or bluman and context procession context procession context procession context procession context 
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodiversity
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                                                                                                                                                                                                                                                  DNA encoding novel human diagnostic protein #5961.
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                                                                                    AAS70157 standard; cDNA; 1512 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT;
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                                                                                                                                                                                                (first entry)
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P-PSDB; ABG05970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                13-FEB-2002
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                                                                                                                                          AAS70157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                 RESULT 12
                                                              AAS70157
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome on gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed egenes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in dispositics, forensics, gene mapping, identification of mutations capposition for generic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS44197-AAS9564 represent novel human configuration, but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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100.0%; Pred. No. 5e-05;
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                                                                DNA encoding novel human diagnostic protein #4571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID No 4571; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631
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13-FEB-2002 (first entry)
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nes 32; Conserv
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                                                                                                                                                                                                                                                           Homo sapiens.
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ID AAS9
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AAS90919 standard; cDNA; 1774 BP

RESULT 13

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Human; cytostatic; antisense gene therapy; screening; protein kinase;
cancer; liver; colon; tumour; inflammation; arthritic synovium; CAMK-XI;
calmodulin kinase; enzyme; RACE; rapid amplification of cDNA end; primer;
                                                               Human CAMK-X1 full length cDNA constructing 5' RACE PCR primer.
                 09-AUG-2002 (first entry)
                                                                                                                                                                                                                                           sapiens.
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δλ
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Codingnostic coding sequences of the invention.

Codingnostic coding sequence of this patent did not appear in the printed experiment in the printed expension in the printed expense in the pri
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                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                             novel human diagnostic protein #26723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 26723; 103pp; English.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0540217
2000US-0649167
                                                               (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                    WO200175067-A2.
                                                                                                                                                                                                                                      Homo sapiens.
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23-AUG-2000;
                                                                                                                DNA encoding
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                                                               13-FEB-2002
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               AAS90919;
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AAD36148/C
ID AAD36
XX
AC AAD36
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AAD36148 standard; DNA; 25

δλ g AAD36148;

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The invention relates to a method for screening biologically active agent that modulates cancer associated protein kinase function. The invention also relates to a method for diagnosing cancer comprising determining the upregulation of expression of a nucleic acid sequence encoding a protein kinase. The method is useful for diagnosing cancer. A protein kinase is useful for screening biological agents that modulate cancer associated protein kinase function. Downregulating the activity of protein kinase is useful for inhibiting the growth of a cancer cell, e.g. liver or colon cancer. A nucleic acid encoding protein kinase is useful for inhibiting the growth of a cancer cell, e.g. liver or colon cancer. A nucleic acid encoding protein kinase is useful to screen biopsy cancer. A nucleic acid encoding protein kinase is useful to corresponding mRNA cancer and inflammatory samples such as arthritic synovium, for amplified DNA in the cell or increased expression of corresponding mRNA or protein and is also useful to detect differences in expression levels two cells. The present sequence is 5' rapid amplification of cDNA ends (RACE) pcr. primer used for constructing human calmodulin kinase CAMK-XI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing cancer, comprises determining the upregulation of expression of a nucleic acid sequence encoding a protein kinase or upregulation of expression of the protein kinase, in the cancer \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The present sequence referred as SEQ ID NO: 17 is also shown in page 25 of the specification but lacks two bases at the 5^{\prime} end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 82; 87pp; English.
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Conservative 0;
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                                                                                                                                                                                                                  2000US-233999P.
2000US-237419P.
2000US-237423P.
2000US-238558P.
2001US-290555P.
                                                                                                                                                 20-SEP-2001; 2001WO-IB02237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KINE-) KINETEK PHARM INC
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es 25; Conserv
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WO200224947-A2.
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04-OCT-2000;
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02-OCT-2000;
                                                                        28-MAR-2002.
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OM nucleic - nucleic search, using sw model

Run on:

March 14, 2003, 15:22:10 ; Search time 7161 Seconds
 (without alignments)
 9444.779 Million cell updates/sec

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1 tggagtgggagctcaagcag......tttttctctaaaaaaaaa 2447 OLIGO_NUC Gapop 60.0 , Gapext 60.0 Scoring table: Sednence:

Perfect score:

2054640 seqs, 14551402878 residues Searched:

0 Word size :

4109280 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

GenEmbl:* Database :

9b_ba:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

Sequence 3 from Patent W00224947. RESULT 1
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KEYWORDS
SOURCE
ORGANISM

PAT 06-JUN-2002

linear

DNA

AX399682.1 GI:21335455 human.

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE AUTHORS TITLE JOURNAL

Delaney, A.D. and Yoganathan, T. Cancer associated protein kinases and their uses Patent: WO 0224947-A 3 28-MAR-2002;

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Contact: MGC help desk
Manil: gapbs-rémall.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
                                                                                                                  TACCCAGACTCCCACTCTGCACACTCACTCCCACCTCTCAAGCCTCCAACCTCTTGGC
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                                                                        TGGTGGTCTGCCTGTGAGCTCTTCAAGTTCTAATCCTTAACTCCAGGATTAGCTCCCAAG
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Strausberg, R.
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VNGSLHISSSLVPMHQGSLAAGPCGCCSSCLNIGSKGKSSYCSEPTLLKKANKKQNFK
SEVMVPVKASGSSHCRAGQTGVCLIM"
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14196444.
Contact: nisc_more in the contact is a backstrom-Sternberg, S.M., Benjamin, B., Batkseley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haphighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, O.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McCowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Ysurgeon, C., Vogt, J.L., Malker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
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/lab_host="DH10B"
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iive 0; Mismatches
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/organism="Homo sapiens"
/db_xref="LocusID:57172"
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CAGCITGTICTGGTGGGGAGCICITTGACCGGAICCTGGAGCGGGGTGTCTACACAGAG	AAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAATACCTACATGAGAT 	GGCATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCTTACCTTACCCTGAAGAGAACCIIIIIIIIII	TCTAAGATCATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGGCATCATGTCC	ACTGCCTGTGGGACCCCAGGCTACGTGGCTCCAGAAGTGCTGGCCCAGAAACCCTACAGC	AAGGCTGTGGATTGCTGGTCCATCGGCGTCATCACCTACATATTGCTCTGTGGATACCCC	CCGTTCTATGAAGAAACGGAGTCTAAGCTTTTCGAGAAGATCAAGGAGGGCTACTATGAG 	TITGAGICICCAITCIGGAIGACAITICIGAGICAGCCAAGGACITIAITTGCCACTIG	CTTGAGAAGGATCCGAACGAGCGGTACACCTGTGAGAAGGCCTTGAGTCATCCCTGGATT	GACGGAAACACGGCCTCCACCGGGACATCTACCCATCAGTCAG	AACTTTGCTAAGAGCAAGTGGAGGCAAGCCTTCAACGCAGCAGCTGTGGTGCACCACATG	AGGAAGCTACACATGAACCTGCACAGCCCGGGCGTCCGCCAGAGGTGGAGAACAGGCCG	CCTGAAACTCAAGCCTCAGAAACTCTAGACCCAGCTCCCCTGAGATCACCATCACCGAGGIIIIIIIIII	GCACCTGTCCTGGACCACAGTGTAGCACTCCCTGCCCTG	GGCCGCCGGCCCACTGCCCCTGGTGGCAGGTCCCTCAACTGCCTGGTCAATGGCTCCTC	CACATCAGCAGCAGCCTGGTGCCCATGCATCAGGGGTCCCTGGCCGCGGGGCCCTGTGGC	TGCTGCTCCAGCTGCCTGAACATTGGGAAGGAAAGTCCTCCTACTGCTCTGAGCCC	ACACTCCTCAAAAAGGCCAACAAAAACAGAACTTCAAGTCGGAGGTCATGGTACCAGTT	AAAGCCAGTGGCAGCTCCCACTGCCGGCAGGCAGACTGGAGTCTGTCT
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PRI 15-JUL-2002 moderately

AK095713 2612 bp mRNA linear Homo sapiens cDNA FLJ38334 fis, clone FEBRA2007534, salmlar to CamKI-like protein kinase. AK095713.1 GI:21755035

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Homo sapiens calcium/calmodulin-dependent protein kinase I gamma
(CAMK1G) mRNA, complete cds.
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AF428261.1 GI:16755791
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KEYWORDS
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ORGANISM

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2464)
Schutte, B.C., Bjork, B.C., Coppage, K.B., Malik, M.I., Gregory, S.G., Scott, D.J., Brentzell, L.M., Watanabe, Y., Dixon, M.J. and Murray, J.C.
A preliminary gene map for the Van der Woude syndrome critical region derived from 900 kb of genomic sequence at 1q32-q41
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numan ortholog
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                                                                                                                                       2 (bases 1 to 2464)
Bjork, B.C., Watanabe, Y., Murray, J.C.
Characterization of the human orthol
(CamKig) at 1432-441
Unpublished
3 (bases 1 to 2464)
Bjork, B.C., Watanabe, Y., Murray, J.C.
Direct Submission
Submitted (05-0CT-2001) Genetics, Un
Iowa City, IA 52242, USA
Location/Qualifiers
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73. 1503
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327	384	444	504	564	624	684	744	804	864	924	984	1044	1104	1164	1224	1284	1344	1404
QQ	Qy	Qy	oy Ob	O.Y DD	Qy Db	QY Dp	Qy Db	Qy Dp	Qy Db	Qy Db	Oy Db	Qy Dp	Qy	Qy	Qy Db	Qy Db	Qy Dp	ОУ

2363 2423 2063 2123 2243 2245 2303 2305 2425 1526 1643 1825 1883 2003 2005 2065 2183 2185 2365 1884 TGTGTCACCTTCTCCAAGCAAAGCCATATGGAGCATCTACCCAGACTCCCACTCTGCACA 1943 CAGTITCCTCGCCCTCCACCCCTCCAGCTTCATGCTCAGTTGTGCTTAATAAAATGGA 1407 AAAACAGAACTTCAAGTCGGAGGTCATGGTACCAGTTAAAGCCAGTGGCAGCTCCCACTG 2006 TGCCTGCCCATCTGCATGAATGACAGGCAGCTCCCCATGGTGGTCTTGCCTGTGAGGTCTTT CACACACCCAATGGAGTTAACCTTGGAAGTTGACTATTTTAATGTCTGCCAGGAGTTCTA ATCCTGCCTCTGTTCCCCTTTTCTCCTTGAAAGTCCAGCACACCATTCTTGTCCTTCCC GCAGAGGAGGAAGGCAGAGCAAGTGGAGCAGGGCTTAGCAGGAGCAGTTTCTGGCCAGA CCCTGACCTGCCTCTATGCCCCACACACCTACGTGCCGTGGCTCTGTGCAGTGCTACGT AGATAGCTCTCGCCTGGGTCTGTGTGTTTGTCGTGAAAAGCTTAATGGGCTGGCCAGGC TGCCTGCCCATCTGCATGAATGACAGGCAGCTCCCCATGGTGGTCTGCCTGTGAGCTCTT CTTCTGGCCCTTCTCCCTGCCTCAATCTAAAAGCAGTGCCACACCCTCCAAAGTGGAATA GAAAGAAGTTCATGAGTAAGGGCTGCAAGGAATTCTTATCCTGGCCACATGTCCTCCGTG 1944 CACTCACCTCCCACCTCTCAAGCCTCCAACCTCTTGGCCAGATTGGGCTCATTAATGTCGT CCGGGCAGGCCAGACTGGAGTCTGTCTCATTATGTGATTCCTGGAGCCTGTGCCTATGTC CATATTTTCTCTAAAAAAAA 2447 1524 1647 1707 2004 2064 2066 2124 2126 2184 2244 2304 2306 2364 2366 2424 2426 1467 1527 1587 1644 1704 1764 1824 1464 1584 Вþ a 0.5 0.5 0.5 0.5 0.5 QY Db οy g δ ŏ 0y 0y 0y 0b QΥ g Qy Db oy Oy Ob

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VKQRLTGKLFALKCITKKSPAFRDSSLENEIAVLKKITKHENTYLEDITESTTHYYLVM
QLVSGGELFORLLERGVYTETDASLVLOQVLSAVKYLHENGIVHRDLKPENLLYLTPE
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SLNCLVNGSLHISSSLVPMHQGSLAAGPCGCCSSCLNIGSKGKSSYCSEPTLLKKANK
          21-APR-1999
                                                                                                                                                                                                           of at
                                                                                                                                                         Direct Submission
Submitted (21-APR-1999) E-mail contact: humquery@sanger.ac.uk
This sequence was generated from CDNA clones isolated using
sequence from the bacterial clone 272L16 (AL023754) and EST data.
The EST sequences listed match this sequence with an identity of eleast 95% between the coordinates shown.

Further information can be found at
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1738)
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764 . .842
http://www.sanger.ac.uk/HGP/Chrl/ Partial, experimentally determined gene.
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                                                                                                                                                                                                                                                                     Sanger Centre name: dJ272L16.Cl.1.
Location/Qualifiers
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843. .930
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TCCAGAAGAACTTTGCTAAGAGCAAGTGGAGGCAAGCCTTCAACGCAGCAGCTGTGGTGC 1012
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                                                                  113 AGACCACCAACATCCGGAAAACCTTCATTTTATGGAAGTGCTGGGATCAGGAGCTTTCT
                                                                                                                         CAGAAGTTTTCCTGGTGAAGCAAAGACTGACTGGGAAGCTCTTTGCTCTGAAGTGCATCA
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  Length 1738;
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Pred. No. 0;
0; Mismatches
  66.9%;
99.9%;
                             Conservative
              Best_Local Similarity
Matches 1736; Conserv
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HS272L16
Hwan DNA sequence from clone 272L16 on chromosome 1q32.1-32.3.
Contains the 3' end of the LAMB3 gene for Laminin, Beta 3 (Nicein, Kalinin, BM600) and a novel Rat Ca2+/Calmodulin dependent Protein Kinase LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D1S491
AL023754. GI:4007152
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Submitted (27-NOV-1998) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E.mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Dec 12, 1998 this sequence version replaced gi:3873472.
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              HTG; BM600; ca repeat polymorphism; Ca2+/Calmodulin dependent
Protein Kinase; D1S491; Kalinin; LAMB3; Laminin Beta 3; Nicein.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 157875)
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Homo sapiens
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JOURNAL
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlapp as described above. This sequence is the entire insert of clone 272L16. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                         272116 is from the library RPCII constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.mad.buffalo.edu/ VECTOR: pCYPAC2 This sequence was generated from a human chromosome 1 bacterial clone contig constructed in collaboration by the Sanger Centre chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                          I mapping group and Brian Schutte, Bryan Bjork, Kevin Coppage and Jeffrey Murray. Department of Pediatrics, University of Iowa, USA. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .365 of consensus"
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10108. .10282
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/note="MIR repeat: matches 56. .142 of consensus"
8020. .8067
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8380. .9083
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/note="LTR7 repeat: matches 1. .450 of consensus"
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/note="MLT1A2-internal repeat: matches 358.
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/note="MLT1A1-internal repeat: matches 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          966. .1078
/note="MLT11 repeat: matches 281. .410 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    460. .6781 'note="MLT1A1 repeat: matches 1. .318 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .711 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MLT1A1 repeat: matches 318.
6020, .6459
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10929. .11005
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8150. .8293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
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/note="MSTD repeat: mat
1585. .1875
/note="MLTIA1 repeat: m:
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/note="MER34 repeat: 13090. .3417
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/clone="RP1-272L16"
/clone_lib="RPCI-1"
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repeat_region

repeat_region	te="L2 repeat: matches 26712748 o 9212129
repeat_region	~~
repeat_region	/note="9 copies 4 mer acac 86% conserved" 12722, .12855
epeat redi	/note="MER91A repeat: matches 20186 of consensus" 1310813221
isc_featu	note="MIR repeat: matches 80191 omplement(1356313979)
repeat_region	AQU/545/ AQU/6848"
repeat_region	repeat: matches 60105 of consensus" 442
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erections	. [
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1 6 6	-
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epear_reg	1946019871 /note="L2 repeat: matches 23092748 of consensus"
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repeat_region	20200, .20228 // // // // // // // // // // // // //
repeat_region	.20365 "MER34 repeat: matches 413 .543 of
repeat_region	.20388 .1mb30 roomst. matches ARA 503 of conson
repeat_region	uinza repear, marchies 404,
repeat_region	repeat: matches 2366 of consensus
	/note="MER34 repeat: matches 6172 of consensus" 2183422278
4	/note="Millo repeat: matches 1466 of consensus"
r fier rada	//note="26 copies 2 mer ag 79% conserved"
epeat_regi	2282622937 /note="MER81 repeat: matches 1112 of consensus"
repeat_region	2489725034 /note="MER5A repeat: matches 30171 of consensus"
_reg	.25193 "MIR repeat:
repeat_region	2520725435 /note="MIR repeat: matches 13259 of consensus"
repeat_region	2591926363 /note="MLTIF repeat: matches 68541 of consensus"
repeat_region	2636426813 /note="MER4A2 repeat: matches 1503 of consensus"
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repeat_region	.27357 1.2 repeat: matches 2292 2723 o
repeat_region	27820
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repeat region	/note="10 copies 4 mer caca 100% conserved" 29036, .29195
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JOUGE "FLAME repeat: matches 7. .142 of consensus" 30246. .30440. A repeat: matches 683. .874 of consensus" 30246. .30440. .30440. .30440. .30440. .30440. .30440. .30440. .30440. .30481. .874 of consensus" 30789. .30789 .30789 .31090. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31060. .31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 147616 GCTGCCAGCGGGCAGCCCCTCATAGGAGGCCCCAGGAGGCAGCGCAAGGCGTAGAAGCC 147675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147916 ACCTCTCAAGCCTCCAACCTCTTGGCCAGATTGGGCTCATTAATGTCGTTGCCCTGCAA 147975
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Pred. No. 0;
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/note="HAL1 repeat: matches 355.
30095. .30228
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Lilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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Page 11

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TEALSTALDIO MERREEDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRV
TCKLFALKCIKKSPAFRDSSLENEIAVLKRIKHENIYTLEDIYESTTHYYLVMQLVSG
GELFDRILLERGVYTEKDASLVIQQVLSAVKYLHENGIVHRDIKPENLLYTPEENSKI
MITDFGLSKMEDNGVWSTACGTPGYNAPEVLAQKPYSKAVDCWSIGVITYILLGGYP
FYEETSKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALRHPW
TOGTALHBYDIYPSVSLOIQKNFAKSKWRQAFRAAVVHHWKLHMNLHSPSVRQEVE
NRPPVSPAPEVSRPDSHDSSITEAFILDPSTPLPALIRLPCSHSSRPSAPSGGRSLNC
LVNGSLRISSSLVPROGOFLARGPCGCCSSCLNIGNKGKSSYCSEPTLFRKANKKONF
KSEVWRYKAGGSTHGRGGTGCVLW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 41 Row: i Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene
                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 2416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.
                                                                                                                                                                                      Strausberg_R.
Direct Submission
Submitted (18-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
      complete cds
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                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) By Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="mus musculus"
/db_xref="taxon:10090"
/clone="mGC:30513 IMAGB:4502479"
/tissue_type="Eye, retina, mouse strain C57Bl\6"
/clone=lib="NHH MGC_94"
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/protein_id="AAH21840.1"
/db_xref="GI:18256867"
Mus musculus, clone MGC:30513 IMAGE:4502479, mRNA, BC021840
BC021840.1 GI:18256866
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                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
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100.0%; Pred. No. 9.2e-29;
iive 0; Mismatches 0;
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Matches 71; Conserva
                                                                                                             Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prediction.
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AUTHORS
TITLE
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                                                                KEYWORDS
SOURCE
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                                                                                                    Db 148276 GTTCCCTTTCTCTCTTGAAAGTCCAGCACATTCTTGTCCTTCCCCAGTTTCTTCT 148335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 148336 CCTCCACCCTCCAGCTTCATGCTCAGTGTTGTGCTTAATAAAATGGACATATTTTCT 148395
                                     Db 148036 CCTTAACTCCAGGATTAGCTCCCAAGTGCGCTGAGACCCAGCACCCAGCACACTCTGGCCCT 148095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                  148216 TGGAGTTAAACCTTGGAAGTTGACTATTTTAATGTCTGCCAGGAGTTCTAATCCTGCCTCT 148275
                                                                                                                                                                                                                                                                                                                                                                                                                                              2375 CCCTCCACCCTCCAGCTTCATGCTCAGTGTTGTGCTTAATAAAATGGACATATTTTTCT 2434
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                    2195 ATGAGTAAGGGCTGCAAGGAATTCTTATCCTGGCCACATGTCCTCCGTGCACACACCAA
                                                                                                                                                                                                                                                                         2255 IGGAGTIAACCTIGGAAGTIGACTATITIAATGTCTGCCAGGAGTTCTAATCCTGCCTCT
                                                                                                                                                                                                                                                                                                                                                              GTTCCCTTTTCTCTCTCTTGAAAGTCCAGCACCATTCTTGTCCTTCCCCAGTTTCCTCG
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100.0%; Pred. No. 7.7e-33;
ive 0; Mismatches 0;
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Weston, M.D. and Kimberling, W.J.
A new polymorphism for the DLS70 locus
Unpublished (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319
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dinucleotide repeat polymorphism.
Homo sapiens DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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/rpt_type=tandem
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748. .771
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Unitect boundaries of the comparing the comparing of the comparing sequence assembly data is compared from overlapping clones. More differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by the resolve all sequencing problems, such as compressions and repeats; all regions were covered by as compressions and repeats; all regions were covered by as compressions are used to associate primary accession numbers given in the feature table with their source databases: Ems. EMBL; Sw.; SWISSPROT; TI:, TREMBL; WP:, WORMPEP; Information on the WORMPEP that their 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACO22675 184754 bp DNA linear HTG 09-MAY-2001
Mus musculus clone RP23-59N15, WORKING DRAFT SEQUENCE, 13 unordered
pieces.
                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 182054)
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from the RPCI-23 Mouse PAC Library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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AC022675.3 GI:13940729
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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hes 0;
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Web site: http://mrcseq.har.mrc.ac.uk
Contact: mouseq@har.mrc.ac.uk
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44402 c 42300 g 46197 t
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/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="1"
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CT 84830
                                                                                                                                                                                                                   Kay, M.
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AL365314
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MITDFGLSKMEQNGVMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPP
FYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALRHPW
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NRPPVSPAPEVSRPDSHDSSITEAPILDPSTPLPALTRLPCSHSSRPSAPSGGRSLNC
LVNGSLRISSSLVPMQQGPLATGPCGCSSCLNIGNRGKSSYCSEPTLFRRANKKQNF
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/translation="MGRKEEEDCSSWKKQTINIRKTF1FMEVLGSGAFSEVFLVKQRV
TGKLFALKCIKKSPAFRDSSLENEIAVLKRIKHENIVTLEDIYESTTHYYLVMQLVSG
                                                                                                                          ROD 07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2427)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bjork, B.C., Watenabe, Y., Murray, J.C. and Schutte, B.C.
Characterization of the human ortholog of rat CaM Kinase I gamma (CaMKI) at 1q32-q41
Unpublished
(bases 1 to 2427)
Bjork, B.C., Watenabe, Y., Murray, J.C. and Schutte, B.C.
Direct Submission
Submitted (05-0CT-2001) Genetics, University of Iowa, 140 EMRB, Iowa City, IA 52242, USA
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                                                                                                                          AF428262 2427 bp mRNA linear ROD 07-NOV-29
Mus musculus calcium/calmodulin-dependent protein kinase I gamma
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/clone="TMAGE:4502479"
/clsue_type="retina"
/note="corresponds to EST BG293660"
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Local Similarity 100.0%; Pred. No. 9.2e-29;
Nes 71; Conservative 0; Mismatches 0;
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694 c 601 q 547 t
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/db_xref="taxon:10090"
/chromosome="1"
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86. .1519
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D86557
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SOURCE
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                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: WIRR
Web Site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact clone name: 15039
Contact clone name: 15039
Contact clone name: 15039
Sequencing vector: M13: M77815; 22% of reads
Consensus quality: 179992 bases at least Q40
Consensus quality: 179992 bases at least Q40
Consensus quality: 181970 bases at least Q20
Insert size: 182000; garnose-fp
Consensus quality: 18276 bases at least Q20
Insert size: 18354; sum-of-contigs
Quality coverage: 12.8 in Q20 bases; agarose-fp
Quality coverage: 12.8 in Q20 bases; agarose-fp
Quality coverage: 12.8 in Q20
**NOTE: This is a 'working draft' sequence record is
** runs of N, but the exact sizes of the gaps are unknown.
** This record will be updated with the finished sequence
** as soon as it is available and the accession number will
** be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (06-FBB-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA ON MAY 4, 2001 this sequence version replaced gi:7657723. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4355 4454; gap of 100 bp 4355 4454; gap of 100 bp 4555 4454; gap of 100 bp 4555 5468 5567; gap of 100 bp 5568 567; gap of 100 bp 6718 6817; gap of 100 bp 6818 8112; contig of 1295 bp in length 8113 8212; gap of 100 bp 8213 9269; contig of 1057 bp in length 9270 9369; gap of 100 bp 9370 11162; contig of 1073 bp in length 9370 11162; contig of 1073 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              o of 100 bp contig of 1319 bp in length
                                                         1 (bases 1 to 184754)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-59N15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11163 11262: gap of
11263 12581: con
                                                                                                                                                          (bases 1 to 184754)
                                                                                                                                  Unpublished
  ORGANISM
                                                                 REFERENCE
AUTHORS
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TITLE

COMMENT

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linear ROD 07-FEB-1999 partial cds.
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Profein Kinase.
Rattus norvegicus embryo (E18) brain cDNA to mRNA, clone_lib:S. Nakanishi clone:N5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 AACATTGTGACCCTGGAGGACATCTATGAGAGCACCACCACCTACTACTGGTCATGCAG 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1320 others
                                        13893 13992: gap of 100 bp
13993 23297: contig of 9305 bp in length
23298 23397: gap of 100 bp
23389 23920: contig of 15523 bp in length
38921 39020: gap of 100 bp
39021 57984: contig of 18964 bp in length
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                    bp in length
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for Protein Kinase,
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Pred. No. 1.7e-23;
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a 42686 c 43285 g 49746 t
p of 100 bp contig of 1211 k
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/note="assembly_fragment"
12682. .13892
/note="assembly_fragment"
13993. .23297
/note="assembly_fragment"
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/note="assembly_fragment"
58085. .141207
/note="assembly_fragment"
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5568. .6717
/note="assembly_fragment"
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/note="assembly_fragment"
8213. .9269
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9370. .11162
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/note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                       1. .4354
/note="assembly_fragment
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/note="assembly_fragment
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vector_side:left"
13892: cort
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D86557
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                                                                                                                                                                                                                         Vokokura, H.
Direct Submission

Submitted (15-JUL-1996) Hisayuki Yokokura, Nagoya University School

of Medicine, Department of Pharmacology; Tsurumai 65, Showa-ku,
Nagoya, Alchi 466, Japan (Tel:052-744-2075, Fax:052-744-2083)

1. 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Protein Kinase"
/protein_id="BAA19880.1"
/db_xref="G1:2077934"
/translation="MGRKEEEDSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRV
TGKLFALKCIRKESPAFUSSSLEDNEIAYLKRIKHENIYTLEDIYESTTHYYLVMQLVSG
GELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYITPEENSKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MITDFGLSKMBONGVMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPP
FYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALRHPW
IDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFN"
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*** SEQUENCING IN PROGRESS ***,
                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to calcium/calmodulin-dependent protein
kinase I mRNA (L24907, L26288)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "L'bases 1 to 178272)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Britava, M., Brown, E., Brown, M., Bryant, N.P.,
Buday, C., Burch, P., Burkett, C., Burzell, K.L., Byrd, N. C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          778 GAGTTTGAGTCTCCCATTCTGGGATGACATTTCTGAGTCAGCCCAAGGACTTTATTTGCCA 836
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0
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                                                                                  (bases 1 to 1013)
Yokokura, H., Terada,O., Naito,Y. and Hidaka,H.
Yoslation and comparison of rat cDNAs encoding
Ca2+(calmodulin-dependent protein kinase I isoforms
Biochim. Biophys. Acta 1338 (1), 8-12 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; 1
8.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="brain"
/clone_lib="S. Nakanishi"
/dev_stage="embryo (E18)"
<1. 86
87. >1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Rattus norvegicus clone CH230-1D9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.4%; Score 59;
100.0%; Pred. No.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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AC126166
AC126166.2 GI:21700365
HTG: HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="N5"
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                                                                    Rattus.
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hes 59;
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AC126166
LOCUS
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SOURCE
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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 76 contigs. The true order of the pieces

* is not known and thair order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Worley, K.C.
Direct Submission
Submitted (31-70L-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77039, USA
On Jul 6, 2002 this sequence version replaced gi:21693754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (04-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 178272)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990329 consensus quality: 113604 bases at least Q40 consensus quality: 121900 bases at least Q30 consensus quality: 127034 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center clone name: CH230-1D9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- Genome Center
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Worley, K.C.
Direct Submission
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1071: contig of 1071 bp in length

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length
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                 Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlson, E., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L. Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Loulseged, H., Lozado, R.J., Lu, X., Lucier, R., Martinez, E., Massey, E., Mawhiney, E., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., Mcced, M.P., Mordson, M., Norgan, M., Neal, G., Metcker, Morgan, M., Norgan, M., Ren, Y., Riwes, M., Rojas, A., Pamers, M., Stanley, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, M., Sasson, I., Sotetk, A., Tabor, P., Tamerisa, A., Tamerisa, M., Thomas, S., Warten, K., Wasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Walliams, G., Williamson, A., Waleczyk, R., Wooden, S., Worley, K., Weinster, S., Marren, R., Wand, C., Wulliams, G., Williamson, A., Waleczyk, R., Wooden, S., Worley, K., Weinster, Shmission
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NOTE: This is a 'working draft' sequence. It currently consists of 71 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                    Submitted (07-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 191584)
                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (132-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 18, 2002 this sequence version replaced gi:20522179.

Center: Baylor College of Medicine
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
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2121: gap of unknown length
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Submitted (10-CCT-2001) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/product="Similar to calcium/calmodulin-dependent protein
kinase I"
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This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
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                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
/map="FVB/N"
/map="PVB/N"
/clone="MGC:18933 IMAGE:3969343"
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/db_xref="GI:15928726"
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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March 15, 2003, 04:12:52 ; Search time 2223 Seconds
   (without alignments)
   3467.860 Million cell updates/sec
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Listing first 45 summaries
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Command line parameters:
-MODEL=frame+_D2n_indel_-DEV=xlh
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-O-/cgn2_1/USPTO_spool/US09960643/runat_07032003_090517_19885/app_query.fasta_1.647
-DB=EST -QFWT=fastap -SUFFIX=p2n_rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-OCALIGN=200 -FRR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -AAXLEN=200000000
-USER=US09960643_GCM_1_1996_Grunat_D7032003_090517_19885 -NCPU-6 -ICPU=3
-NO_XIPXY -NO_MMAP -LARGEQUERY -NGS_CORS=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_ITMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RES	Description	BM547443 AGEN	BI821474 60303	BI77262	AL560091	BI82448	BM92133.	BI75303	BG29366 BG71592	BQ94962	AW25122-	BM94441	BQ086333 BM91926	BG16866	BI83463: BI75846	BE56954	BQ066920	AW826803	BM05143	B154554 AW25405	BG70227	B1463145 6U3 A1595095 ml34	BI756289 603	BG302505 IL3 BE266955 601	AL578723 AL57	AW52222 BI75746	BM728430 UI-	BF582563 602 BF143967 601	BG895406 358	BQ897490 AGE	BM903/1 BI76126	BG307424 fm03h03.	ENTS	bp mRNA linear EST 20-FEB-2002 Homo sapiens cDNA clone IMAGE:5724450			Oranists. Voxtobrats. Butalocatomi.	Catarrhini; Hominidae; Homo.	//. Manmalian Gene Collection (MGC)
SUMMARIE	ID	BM547443 BO934044	BI82147	BI77262	AL560091	BI82448	BI81826	BI75303	BG29356	BQ94962	AW251224 AT.556476	BM94441	BQ08633	BG16866	BI83463	BE56954	BQ06692	AW82680:	BM05143	AW25405	BG70227	B1463143 A1595095	BI75628	BE26695	AL578723	BI75746	BM72843(BF58256	BG89540	BQ89749(BI76126	BG30742	ALIGNMENT	1126 _MGC_125		13		Primates;	i.nih.gov/ f Health, 1
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/do_xref="taxon:9606"
/done="IMAGE:5724450"
/clone="IMAGE:5724450"
/clone="IMAGE:108"
/dob host="DHIOB"
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Site_1: EcoRV (destroyed); Site_2: Noti; RNA source pool of three ovaries, from females ranging in age from 38 to 69 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kD, insert size range 1.3.5 kD. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."
               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12713 row: 1 column: 19
High quality sequence stop: 623.
Location/Qualifiers
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Mouse mouse.

Mus musculus.

Mus musculus.

Musmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 905)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1029 GAAGCTACC-CTGAACCTGGACAGCCGGGAATTCCNNCCCCAAAAGGGGGGAAACAGGCC 1087
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                                                                                     AspCysTrpSerIleGlyValIleThrTyrIleLeuLeuCysGlyTyrProProPheTyr
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Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
El (Abases I to 809)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
contact: Robert Stravayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMII47 row: c column: 17
High quality sequence stop: 808
Location/Qualifiers
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Primer: Oligo dT. Average insert size 1.95 kb.
Constructed by ResGen, Invitrogen Corp. Note: this is
NIH_MGC Library.
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E 1 (Dasses 1 to 812)

IN 1H-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Likl at: http://image.llnl.gov
Plate: LiAMI157 row: m column: 20

High quality sequence start: 2

High quality sequence start: 2

Location/Qualifiers
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603060879F1 NIH_MGC_122 Homo
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/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MCC Library.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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/lab_host="DH10B"
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                                                                                                                                                           HisLeu---LeuGluLysAspProAsnGluArgTyrThrCysGluLysAlaLeuSerHis
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                                                                                                                  mRNA linear EST 05-MAR-2002 sapiens cDNA clone IMAGE:5732298
                                                                                                                                                                                                           Homo Sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                     Dupublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Blosscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12734 row: c column: 19
High quality sequence start: 11
High quality sequence start: 11
High quality sequence stop: 651.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism-"Homo sapiens"
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/lab_host="DH10B"
                                                                                                                  BM807335
AGENCOURT_6575096 NIH_MGC_124 HOMO
                                       AspProAsnGluArgTyrThrCysGluLys 270
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AL560091 ALI_FL011_BC1 Homo sapiens cDNR clone CSODG002XN16 5 prime
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1051)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Fall-length cDNA libraries and normalization
Contact: Genoscope
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BP 191 91006 EVRY cedex - France
Emall: seqref@enoscope.cns.fr, Web : www.genoscope.cns.fr.
_Locatien/Qualifiers
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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                                                                                      AL560091.1 GI:12906218
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1158.00
84.29%
72.44%
                                                 mRNA sequence
                                                                                                                                                             Homo sapiens
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Best Local Similarity:
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                                                                 AL560091
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                                                                                                                                       human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 740)

1 (Dases 1 to 740)

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1 National Institutes of Health, Mammalian Gene Collection (MGC)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 IleMetIleThrAspPheGlyLeuSerLysMetGluGlnAsnGly---IleMetSerThr 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              711 GCCGTTGACTGCTGGTCCATCGGAGTGATTGCCTACATCTTGCTCTGCGGGCTACCCGSCT 770
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AlaSerLeuVallleGlnGlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIle 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PheTyrGluGluThrGluSerLysLeuPheGluLysIleLysGluGlyTyrTyrGluPhe 238
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5179957"
/clone_lib="NIH_MGC_115"
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Location/Qualifiers
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BI824483.1 GI:15936033
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AUTHORS
TITLE
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COMMENT
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                                        ACCESSION
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/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
pCWV-SPORT6. Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age for Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1:8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."
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222
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1
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                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                              5.37e-107
1147.00
99.55%
45.64%
                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
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RESULT 8

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//note="Organ: pooled brain, lung, testis; vector:
pcMv-SPORT6; Site_1: NotI; Site_2: EccRv (destroyed); RNA
source anonymous pool of male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EccRv site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C
Gruber (Invitrogen). Research Genetics tracking code
1021. Note: this is a NHLMGC Library."
bp mRNA linear EST 12-MAR-2002
Homo sapiens cDNA clone IMAGE:5753010
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1068)
NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM12788 cov: b column: 19
High quality sequence stop: 592.
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Conservative:
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Indels:
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Thypes:5753010"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
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1068 b
AGENCOURT_6708041 NIH_MGC_115
6, mbm ------
                                                                              BM921532.1 GI:19371911
EST.
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1140.50
94.67%
93.85%
45.38%
                                               5', mRNA sequence.
BM921532
                                                                                                                                                             Homo sapiens
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Query Match:
DB:
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(1-742)
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1134.00
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99.10%
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Best Local Similarity:
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BI753035
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1. (bases 1 to 742)

2. National Institutes of Health, Mammalian Gene Collection (MGC)

3. National Institutes of Health, Mammalian Gene Collection (MGC)

4. Unpublished (1999)

5. Contact: Robert Strausberg, Ph.D.

6. Contact: Robert Strausberg, Ph.D.

7. Contact: Robert Strausberg, Ph.D.

7. Contact: Robert Strausberg, Ph.D.

8. Contact: Robert Strausberg, Ph.D.

8. Contact: Robert Strausberg, Ph.D.

8. C
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Abganism="Homo sapiens"
Abganism="Homo sapiens"
Abganism="Homo sapiens"
Actione="InAGE:5173587"
Actione="InBane"
Abback="DH10B"
Anote="Organ: pooled brain, lung, testis; Vector:
Abgary Sprayer; Site_1: Not!: Site_2: Ecorv (destroyed): RNA source anonymous pool of 6 male brains, age range 23-27; Inale lung, age 27; and 1 male testis, age 69. Library is
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http://mage.lhnl.gov
Plate: LLAM11432 row: d column: 04
High quality sequence stop: 742.
Location/Qualifiers
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BI753035

731 bp mRNA linear EST 25-SEP-2001

603025844F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5196323 5',

mRNA sequence.

BI753035
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oligo-dr primed and directionally cloued (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb, Library is normalized and enriched for full-length clones and was constructed by Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
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                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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Mon Mar 17 12:14:44 2003

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US-09-960-643-2 (1-476) x BG293660 (1-818)
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VERSION
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                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 731)
                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapba-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM11491 row: 9 column: 12
High quality sequence stop: 729.
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                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism="Homo sapiens"
/db_xxef="taxon:9606"
/clone="IMAGE:5196323"
/clone=lbb="NHHMGC_114"
/lab_host="DH10B"
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BG293660 818 bp mRNA linear EST 21-FEB-2001
602390529F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4502479 5',
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAm10311 row: i column: 08
High quality sequence stop: 765.
Location/Qualitiess
Location/Qualitiess
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 818)
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/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                             613 ACCCCAGGCTACGTGCTCCAGAAGTGCTGGCCCCAGAAACCCTACAGCAAGGCTGTGGAT 672
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LeuValIleGlnGlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIleValHis 141
                         182 ThrProGlyTyrValAlaProGluValLeuAlaGlnLysProTyrSerLysAlaValAsp
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Conservative:
Mismatches:
Indels:
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/db_xref="taxon:10090"
/clone="IMAGE:4502479"
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94.69%
93.06%
43.89%
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Alignment Scores:
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NIH-WGC http://mgc.nci.nih.gov/.
NIH-WGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rfmail.nih.gov
Tissue Procurement: Millos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                               LysThrPhellePheMetGluValLeuGlySerGlyAlaPheSerGluValPheLeuVal
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMJ0688 row: e column: 17
High quality sequence stop: 766.
Location/Qualifiers
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Conservative:
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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AW251224.1 GI:6594815
EST 17-DEC-1
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                           21 LysThrPheIlePheMetGluValLeuGlySerGlyAlaPheSerGluValPheLeuVal 40
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostu
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
MetGlyArgLysGluGluAspAspCysSerSerTrpLysLysGlnThrThrAsnIleArg
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AGENCOURT_8744314 Lupski_sclatic_nerve Homo sapiens cDNA clone
BO949629
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Not1: Site_2: Sal1; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCCCCCCG-3' and
5'-GACTAGTTCTAGATCGCGAGCGGCCCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                        I (Marsa 1 to 210)

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Proturement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

thtp://image.libl.gov

plate: LLAM13629 row: g column: 20

High quality sequence stop: 697.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/sex="male"
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Mismatches:
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/dev_stage="adult, 70 yr"
/lab_host="DH10B"
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Matches:
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/db_xref="taxon:9606"
/clone="IMAGE:6205867"
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Euteleostomi;

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Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
                                              451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 PheGluLysIleLysGluGlyTyrTyrGluPheGluSerProPheTrpAspAspIleSer 247
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                      Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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Matches:
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Mismatches:
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98.37%
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                                         University of Iowa
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/u. 90cganism="Homo sapiens"
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/tissue_type="placenta"
/fissue_type="placenta"
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/note="weetor: pCmVsPoRT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVsPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

18 a 263 c 293 g 185 t 3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 962)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization (Dnublished (2001) Contact: Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr. Location/Qualifiers
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Sequence 4, Application US/0993464
Publication No. US20030027153A1
GENERAL INFORMATION:
BUBLICANT: MAYER, JOANE
APPLICANT: BARENT, ROY
APPLICANT: BARENC: ALEXANGER
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/LH702 US1
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICANTON NUMBER: US/09/935,464
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT APPLICATION NUMBER: US 09/757,300
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR SEQ ID NOS: 90
SOFTWARE: PatentIn version 3.0
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Sequence 3, Appli
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     Alignment Scores:
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LENGTH: 1738
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2956.529 Million cell updates/sec
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Sequence 1, P
Sequence 3, P
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                                                                                                                             ; Search time 113
                      GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                        nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Percent Similarity: Best Local Similarity:

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Query DB:	Mato	ch:	100.00% 9	Indels: Gaps:	0 0	
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Oy Dp	21	LysThrPhellel 	ellePheMetGluValLeuGlyS 	31ySerGlyAlaPheS 	SerGluvalPheLeuVal	40
Qy Dp	41	LysGlnArgLeuThrG 	lyLys 	LeuPheAlaLeuLysCysIleLysLy: 	SSerProAlaPhe	60
Qy Db	61	Argaspserser!	SerLeuGluAsnGluIle 	GluileAlaValLeuLysLysil 	eLysHisGluAsnIle 	80 257
Qy	81 258	ValThrLeuGlu 	.uaspileTyrGluSerThrThrH 	<pre>fhrThrHisTyrTyrLeu ccacccacTacTacTG</pre>	ValMetGlnLeuval 	100
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oy Dp	121 378	SerLeuVallle(AGTCTGGTGATC(31nGlnValLeuSer 	alavallystyrLeuHisGluAsn 	HisGluAsnGlyIleVal 	140
oy B	141	HisargaspLeul 	euLysProGluAsnLeuLeuTy 	rLeuThrPrc CCTTACCCC	oGluGluAsnSerLysile 	160
Qy Dp	161 498	MetileThraspi 	PheGlyLeuSerLysMet TTTGGTCTGTCCAAGATC	GluGlnAsnGl 	ylleMetSerThrAlaCys 	180
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Oy Dp	201	AspCysTrpSerlle 	IleGlyValIleThrTyrIl 	eLeuLeuCys 	GlyTyrProProPheTyr 	220 677
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Qy Dp	261 798	AspProAsnGlui 	nGluargTyrThrCysGlu 	sGluLysAlaLeuSerHisF 	ProtrpileAspGlyAsn 	280 857
oy Dp	281 858	ThralaLeuHis/ 	euHisArgAspileTyrPro 	YrProSerValSerLeuGlnIleGlnLy 	IleGlnLysAsnPheAla 	300
Oy Db	301 918	LysSerLysTrpArgG 	lnala AAGCC	PheAsnAlaAlaAlaVall 	ValValHisHisMetArgLysLeu 	320 977
Qy Db	321 978	HisMetasnLeu 	HisserProGlyVal 	HisMetasnLeuHisSerProGlyValArgProGluValGluAsnArgPr 	AsnargProProGluThr 	340

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APPLICANT: Meyer, Joanne
APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
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APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martington
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILLE PREFERENCE: 332/1410/2 US1
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT APPLICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-01-09
RINBER OF SEQ ID NOS: 90
SOFTWARE: Patentin version 3.0
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CORGANISM: Homo sapiens
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NAME/KEY: 5'UTR
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                                                                APPLICANT: Bandaru, Rajasekhar TITLE OF INVENTION: 68730 and 69112, Protein Kinase TITLE OF INVENTION: 68730 and 1912, Protein Kinase TITLE OF INVENTION: Molecules and Uses Therefor FILE REFERNCE: MPI2000-521P1R(M)
CURRENT APPLICATION NUMBER: US/10/024,036B
PRIOR FILING DATE: 2001-12-17
PRIOR FILING DATE: 2000-12-22
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Matches:
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'GENERAL INFORMATION:
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Sequence 3, Application US/10024036B

Publication No. US20030028004A1

GENERAL INFORMATION: Rajasekhar

TITLE OF INVENTION: Rajasekhar

TITLE OF INVENTION: Molecules and Uses Therefor

FILE REFERENCE: MPI2000-521P1R(M)

CURRENT APPLICATION NUMBER: US/10/024,036B

CURRENT FILING DATE: 2001-12-17

PRIOR FILING DATE: 2000-12-22

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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Matches:
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Patent No. US20020077459A1

GENERAL INFORMATION:

TITLE OF INVENTION: Action of Action o
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Sequence 1, Application US/09817181

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Sequence 1, Application US/09817181

Sequence 1, Application US/09817181

GENERAL INFORMATION: ACID MUSECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREVER ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREVER INVENTION: THEREVER INS, AND USES TITLE OF INVENTION UNBER: US/09/817,181

CURRENT FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1372
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Query Match: 34.42% Indels: 272 DB: 9 Gaps: 2 US-09-960-643-2 (1-476) x US-09-935-464-1 (1-157875)	272 145909	Qy 291 ISerLeuGlnIleGlnLysAsnPhealaLysSerLysTrpArg	Oy 305 305 Db 146028 AGGGGGTGGGAAAGCTGTTCTGGGCCCCTGGAGGCTGGGCTGGCAGGGGTGACATAAGG 146087	Qy 305 305 305 Db 146088 GCTTCCTGAAATGAGCATTGGAGCTCCGTGTACCCTCTCTGAAATGAGAA 146147	30536 146148 GPGGCCACCACCACAGGGCACAAAGGGAAAGGGAAAGGGAAAGGGCAAAGGCCACAAGGCCT 14	306GlnAlaPheAsnAlaAl 31 146208 CYGAGGTTGCAGAGGCTGGTCTTGTGTCTCTTAGCAAGGCTTCAACGAGC	311 aAlaValValHisMetArgLysLeuHisMetAsnLeuHisSerProGlyValArgPr 33		Qy 351 oGluIleThrIleThrGluAlaProValLeuAspHiSSerValAlaLeuProAlaLeuTh 371	Qy 371 rGlnLeuProCysGlnHisGlyArgArgProThrAlaProGlyGlyArgSerLeuAsnCy 391	Oy 391 sLeuValAsnGlySerLeuHisIleSerSerSerLeuValProMetHisGlnGlySerLe 411	OY 411 UALAALAGIYProCysGlyCysCerSerCysLeuAsnIleGlySerLysGlyLysSe 431	Qy 431 rSerTyrCysSerGluProThrLeuLeuLysLysAlaAsnLysLysGln 447	Oy 447 447 Db 146688 AGCCAAAGATGGAGCCCCAGCTTGGGTCTGAAAGAAATCGGTCAACAGGACTGAAAGAAA	Oy 447	## 0.10000101101000000000000000000000000	Db 146808 AGGGGCAAGGAAAATGCTTCCAGCCCTGTCCCCATCACTACTAGTTGTGAGGCCATTG 146867 Qy 447	Db 146868 ACGAGTCAATGTCTGCTTCTATTTGCTCATCTGTAAACTGGGTTGAAGTCTATTTAC 146927

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                                                                ValThrLeuGluAspIleTyrGluSerThrThrHisTyrTyrLeuValMetGlnLeuVal 100
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150 AAGCAAAGACTGGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCACCTGCCTTC
                                     15 GlnThrThrAsnIleArgLysThrPheIlePheMetGluValLeuGlySerGlyAlaPhe
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                            ArgAspSerSerLeuGluAsnGluIleAlaValLeuLysLysIleLysHisGluAsnIle
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APPLICANT: Olandt, Peter J.
APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN
TITLE OF INVENTION: KINASE FAMILY MEMBERS AND USES THEREFOR
FILE REFERENCE: 10448-017001
CURRENT APPLICATION NUMBER: US/09/797,039
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 60/186,061
PRIOR PILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 13
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Mismatches:
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Matches:
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LeuTyrLeuThrProGluGluAsnSerLysIleMetIleThrAspPheGlyLeuSerLys
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                                               LeuGluArgGlyValTyrThrGluLysAspAlaSerLeuValIleGlnGlnValLeuSer
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1024 GCTTCTGATAAGAACATCAAGGATGGTGTCTGTGCCCAGATTGAAAAGAACTTTGCCAGG 1083
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                                                                                                MetGluGlnAsnGlyIleMetSerThrAlaCysGlyThrProGlyTyrValAlaProGlu 189
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                                                                                                                     :::||| ||||||:::||| CTAGAA GAGCCCTGTGGGACCCCCGAGTATCTGGCCCCAGAG 723
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GTTTACTACAACCGGCTGAAGAACTCGAAGATTGTCATCAGTGACTTCCATCTGGCTAAG
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                                 LeuTyrLeuThrProGluGluAsnSerLysIleMetIleThrAspPheGlyLeuSerLys
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                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Olandt, Peter J.
APPLICANT: Olandt, Peter J.
APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN
TITLE OF INVENTION: KINASE FAMILY MEMBERS AND USES THEREFOR
FILE REFERENCE: 10448-017001
CURRENT APPLICATION NUMBER: US/09/797,039
PRIOR PILING DATE: 2001-02-28
PRIOR PPLICATION NUMBER: US 60/186,061
PRIOR FILING DATE: 2000-02-29
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Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2297
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Patent No. US20020042099A1
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NAME/KEY: misc_feature
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Best Local Similarity:
Query Match:
DB:
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---- IleGlySerLysGl

Mon Mar 17 12:14:43 2003

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Sequence 1, Application US/10153921

Patent No. US2002014243041

GENERAL INFORMATION:

APPLICANT: YAN, Chunhua et al.

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REPERENCE: CLOOG612DIV

CURRENT APPLICATION NUMBER: US/10/15,921

CURRENT APPLICATION NUMBER: 05/202-24

PRIOR APPLICATION NUMBER: 09/734,030

PRIOR FILING DATE: 2000-05-30

PRIOR FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FASTESQ for Windows Version 4.0
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Best Local Similarity:
Query Match:
DB:
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US-10-153-921-1
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Sequence 47. Application US/08935464
Publication No. US20030027153A1
GREERAL INFORMATION:
GREERAL INFORMATION:
APPLICANT: Berrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TITLE OF INVENTION:
DISORDERS SUCH AS SCHIZOPHRENIA
FILE REPERENCE: 3322/1H702 US1
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-09-23
PRIOR FILING DATE: 2001-01-09
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ValSerGlyGlyGluLeuPheAsp-ArgIleLeuGluArgGlyValTyrThrGluLysAs 119
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Publication No. US20020192204A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 15985, A NOVEL HUMAN SERINE/THREONINE
TITLE OF INVENTION: 159865, A NOVEL HUMAN SERINE/THREONINE
FILE REFERENCE: 10448-078001
CURRENT APPLICATION NUMBER: US/09/934,406
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 60,226,740
PRIOR FILING DATE: 2000-08-21
                                                                            470
139
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                                                                                        Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
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; LOCATION: (208)...(2505)
US-09-934-406-1
        FEATURE:

NAME/KEY: misc_feature

CTHER INFORMATION: n=a
US-09-935-464-48
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ORGANISM: Homo sapiens
                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
 ORGANISM: Homo
                                                                 Alignment Scores:
Pred. No.:
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US-09-934-406-1
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Sequence 48, Apolication US/09935464

Publication No. US20030027153A1

GENERAL INFORMATION:

APPLICANT: Meyer, Joane

APPLICANT: Barrington-Martin, Rory

APPLICANT: Barrington-Martin, Rory

APPLICANT: Barrington-Martin, Rory

APPLICANT: Barrington-Martin, Rory

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIP

FILE REFERENCE: 3322/14702 US1

CURRENT APPLICANTON NUMBER: US/09/935,464

CURRENT APPLICANTON NUMBER: US 09/757,300

PRIOR FILING DATE: 2001-01-09

NUMBER OF SEQ ID NOS: 90

SOFTWARE: Patentin version 3.0

SEQ ID NO 48

LENGTH: 470

TYPE: DNA
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Matches:
Conservative:
Mismatches:
Indels:
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        SOFTWARE: PatentIn version 3.0 SEQ ID NO 47
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OF SEQ ID NOS: 90
                                                                        NAME/KEY: misc_feature;
CTHER INFORMATION: n=a
US-09-935-464-47
                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                        TYPE: DNA
ORGANISM: HOMO
                                                                                                                       Alignment Scores:
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US-09-935-464-48
                               LENGTH: 467
                                                                FEATURE
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NUMBER
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Pred. No.: Score: Percent Si Best Local Query Matc).: Similarity: sal Similarity: itch:	1.7e-51 639.50 50.40% 32.00% 25.45%	Length: Matches: Conservative: Mismatches: Indels:	3552 160 92 191 14	
-096-60	-643-2 (1-476)	x US-09-934-40	6-1 (1-3552)		
2 1303	GlyArgLysGluGl GGTGGACCTGAGCT	uAspAspCysSerS TGACCGTTGCATAA	TGTG	Lys aatggaaacagatgctct	14 1362
15	GlnThrThrAsnIl	eArg : ICTT	lePheMetGluValLe ::: :: AAATTGGAAAGGTCAT	LysThrPheIlePheMetGluValLeuGlySerGlyAlaPhe	34
35	SerGluValPheL	erGluValPheLeuValLysGlnArgLeuThrGlyLys: ::	euThrGlyLysLeuPh CCACTGGAAAGGAGTT	SLEUPheAlaLeuLySCysIle 	54
55	LysLysSerProA ::: GACAAAGCCAAAT	laPheArgAspS ::::: GTTGTGGAAAGGAAC	LysLysSerProAlaPheArgAspSerSerLeuGluAsnGlu1leAlaValLeuLy :: GACAAAGCCAAATGTTGTGGAAAGGAACACCTGATTGAGAATGAGATGTGTCAATACTGCG	ulleAlaValLeuLys :::::::: ::: AGTGTCAATACTGCGC	73
74	LyslleLysHisG :::::: CGAGTGAAACATC	yslleLysHisGluAsnileValThrLeuGluA. ::::: :: : GAGTGAAACATCCCAATATCATTATGCTGGTCG.	euGluAspIleTyrGluSerThrThrHi :: TGGTCGAGGAGATGGAACAGCAACTGA	uSerThrThrHisTyr ::: ACAGCAACTGAGCTC	93 1602
94	TyrLeuValMetG ::: TTTCTGGTGATGG	InLeuValSerGlyG :: AATTGGTCAAAGGTG	TyrLeuValMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleLeuGl :::	gileLeuGluArgGly AATTACTTCGTCGACC	113
114	ValTyrThrGluL 	ysAspAlaSerLeuV :: ; GAGATGGCAGTGCCA	ValtyrThrGluLysAspAlaSerLeuVallleGlnGlnValLeuSerAlaValLy: 	LeuSerAlaValLysTyr 	133
134	LeuHisGluAsnGl CTCCATGGCCTCAG	> D	IleValHisargaspLeuLysProGludsnLeuLeuTy 	nLeuLeuTyrLeuThr TCTCTTGGTGTGAA	153 1782
154	ProGluGluA :: TATCCTGATGGAA	snSerLyslleMetI ::: CCAAGTCTTTGAAAC	leThrAspPheGlyLe :: TGGGAGACTTTGGGCT	ProGluGluAsnSerLysIleMetIleThrAspPheGlyLeuSerLysMetGluGln :: :: :: ::: CCTGATGGAACCAAGTCTTTGAAACTGGGGAGACTTTGGGCTTGCGACTGTGGTAGAA	172 1842
173	AsnGlyIleMetSerThrAl ::: GGCCCTTTATACACAGT	erThrAlaCysGlyT ACACAGTCTGTGGCA	hrProGlyTyrValAl cacccacTTATGTGGC	IYIIeMetSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeuAla :::	192 1899
193	GlnLysProTyrS ::: GAAACTGGCTATG	erLysAlaValAspC GCCTGAAGGTGGACA	ysTrpSerileGlyVa ::: TTTGGCAGCTGGTGT	GlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleThrTyrIleLeu :::	212 1959
213	LeuCysGlyTyrP 	roProPheTyrGluG caccaTTCCGAAGTG	.luThrGluSerLy. - 	ysGlyTyrProProPheTyrGluGluThrGluSerLysLeuPheGluLys 	230
231	IleLysGluGlyTyrTy: ATCTTGGCTGGGAAGCT	yrTyrGluPheGluS AGCTGGAGTTTCCGG	GluGlyTyrTyrGluPheGluSerProPheTrpAspAspIleSerGlu:	pIleSerGluSerAla : ::::: .CATCACGGACTCTGCC	250
251	LysAspPhelleCysHis ::: AAGGAATTAATCAGTCAA	AspPheIleCysHisLeuLeuGluLysAspProAsnGlu ::: ::: :: :: GAATTAATCAGTCAAATGCTTCAGGTAAATGTTGAAGCT	<pre>sLeuLeuGluLysAspProAsnGluArgTyrThrCy ::: ::</pre>	ArgTyrThrCysGluLys ::: CGGTGTACCGCGGACAA	270 2139
271	AlaLeuSerHisP ATCCTGAGTCACC	roTrplleAspGlyA ::: ccrGGGrGrCAGATG	aLeuSerHisProfrpileAspGlyAsnThrAlaLeuHisArgAspileTyrP. :: 	gAspileTyrProSer :::::: TAACATGCAAGCTGAG	290
291	ValSerLeuGlnI ::: GTGACAGGTAAAC	leGlnLysasnPhe- ::::::::: TaaaacaGcacTTTa	AlaLysSerLy ATAATGCGCTCCCCAA	ValSerLeuGln1leGlnLysAsnPheAlaLysSerLysTrpArgGlnAlaPhe ::	308 2259

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APPLICANT: Galger, ALEARANGER
APPLICANT: Galger, ALEARANGER
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER.
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: 05/07/96,692
CURRENT PELLOR DATE: 2000-03-01
PRIOR PAPLICATION NUMBER: 60/186,126
PRIOR PAPLICATION NUMBER: 60/200,545
PRIOR PAPLICATION NUMBER: 60/200,545
PRIOR PAPLICATION NUMBER: 60/200,333
PRIOR PAPLICATION NUMBER: 60/200,333
PRIOR PAPLICATION NUMBER: 60/200,333
PRIOR PAPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR PAPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-06-04
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                                                                                                                                                                                                            324 LeuHis------SerProGlyValArgProGluValGluAsnArgProPro 338
                                                                                                                                                                                                                                                                                                                                                                                                                    339 GluThrGlnAlaSerGluThrSerArgProSerSerProGluIleThrIleThrGluAla 358
---LysLeuHisMetAsn 323
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US-09-796-692-7777/c
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115 TyrThrGluLysAspAlaSerLeuValIleGlnGlnValLeuSerAlaValLysTyrLeu 134
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Matches:
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NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7777
LENGTH: 474
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                                                            LOCATION: (10)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (19)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
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633.50
87.90%
75.16%
25.21%
                              TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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Best Local Similarity:
Query Match:
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US-09-796-692-7777
                                                     NAME/KEY: unsure
                                                                                                                                     Alignment Scores:
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Search completed: March 15, 2003, 07:54:16 Job time : 161 secs

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APPLICANT: Bandman, Olga
APPLICANT: Billman, Jennifer L.
APPLICANT: Corley, Nell C.
APPLICANT: Gugler, Karl G.
APPLICANT: Goll, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                US-08-57-1

US-08-55-35-1

US-09-55-35-1

US-09-58-016-1

US-09-58-016-1

US-09-58-016-1

US-09-28-016-1

US-09-38-4

US-09-38-4

US-09-38-4

US-09-38-4

US-09-38-1

US-09-28-016-10

US-08-57-006C-38

US-08-57-006C-39

US-08-57-06C-36

US-08-58-046A-1
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/08878989 Patent No. 5885803 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J J
  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
    USA
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    WODEL-frame+p20.model -DEV-x1h
-Q=CQGD2_LVGSPO_spool_VGS9960643_runat_07032003_090517_19900/app_query.fasta_1.647
-Q=CQGD2_LVGSPO_spool_VGS9960643_runat_07032003_090517_19900/app_query.fasta_1.647
-Q=CQGD2_LVGSPO_spool_VGS9960643_runat_0703003_090517_19000_aum62 -TRANS=human40.cdi
-LOSPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS=human40.cdi
-LISPE45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN-0 -ALIGN=15
-USER-GS09960643_eGGN_1140_etunat_07032003_090517_19900 -NAXLEN-2000000000
-USER-US09960643_eGGN_1140_etunat_07032003_090517_19900 -NCPU-6 -ICPU-3
-NO_XLDXY -NO_MANF -LARGEQPERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XARAPOP=10 -XGAPOP=6 -FGAPOP=6 -FGAPORT=7
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Sequence 1, Appli
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Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                  - nucleic search, using frame_plus_p2n model
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US-09-272-796-12
US-09-713-030-1
US-08-715-568A-2
US-09-529-093A-1
US-09-46-694-3
US-09-800-960-1
US-08-128-446B-16
US-08-128-446B-16
US-09-125-51A-1
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                   273 GCCTTCTCCGAGGTGGTGCTGGCCCAGGAGCGGGGCTCCGCACCTCGTGGCCCTCAAG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 ArgGlyValTyrThrGluLysAspAlaSerLeuValIleGlnGlnValLeuSerAlaVal 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 LysTyrLeuHisGluAsnGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyr 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 GlnAsnGlyIleMetSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 191
                                                                                                                                                                                                                                                                                                                                                      53 Cyslle---LysLysSerProAlaPheArgAspSerSerLeuGluAsnGluIleAlaVal 71
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                                                       INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 1282 base pairs TYPE: nucleic acid STRANDENNESS: single TOPOLOGY: linear
REGISTRATION NUMBER: 36,749
       REFERENCE/DOCKET NUMBER: PF
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-655
TELEFAX: 415-845-4166
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SerLeuGlnIleGlnLysAsnPheAlaLysSerLysTrpArgGlnAlaPheAsnAlaAla 311
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873 CTGAGGGCCAGCTATGAGTTTGACTNTCCTTTCTGGGATGACATCTCGAGAATCAGGCAAA 932
                                          AspPheIleCysHisLeuLeuGluLysAspProAsnGluArgTyrThrCysGluLysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bandman, Olga
APPLICANT: Bandman, Jennifer L.
APPLICANT: Gorley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Gall, Preeti
APPLICANT: Goll, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
WINDER OF SEGUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastED for Windows Version 2.0
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/272,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Incyte Pharmaceuticals, Inc
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APPLICATION NUMBER: 08/878,989
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REGISTRATION NUMBER: 36,749
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TELEPHONE: 415-855-0555
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LENGTH: 1282 base pairs
TYPE: nucleic acid
STRANDEDNES: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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IBM Compatible
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CLONE: 827431
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|GGCAGATCCCA 1151
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APPLICANT: MERKLOV, Gennady
APPLICANT: MERKLOV, Gennady
APPLICANT: MERKLOV, Gennady
APPLICANT: MELY MIG-Hui
APPLICANT: MELY MIG-Hui
APPLICANT: PAN, Chunhua
APPLICANT: YAN, Chunhua
APPLICANT: YAN, Chunhua
TITLE OF INVENTION: TEREACE
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND
FILE REFERENCE: CLOOG612
CURRENT APPLICATION NUMBER: US/09/734,030
CURRENT FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuGluArgGlyValTyrThrGluLysAspAlaSerLeuValIleGlnGlnValLeuSer 129
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 LysLysSerProAlaPheArgAsp-----
    ; Sequence 1, Application US/09734030; Patent No. 6461846; GENERAL INFORMATION:
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747.50
54.91%
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                                      332 GluValGlu 334
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Query Match:
DB:
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                                                                                         RESULT 3
US-09-734-030-1
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                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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|TGCGGGACCTTTGGATCTTTTGGGACACGCTTTGGCAGGACATCTTAGGGTTTGTC
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                                                              Conservative:
Mismatches:
Indels:
                                                                                                                          US-09-960-643-2 (1-476) x US-09-272-796-12 (1-1282)
                                        Length:
Matches:
                                 1.29e-86
990.00
74.928
59.758
                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                         Alignment Scores:
Pred. No.:
US-09-272-796-12
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SETTACTACAACCGGCTGAAGAACTCGAAGATTGTCATCACTGCATCTGGCTAAG 723
                                                            PheTrpAspAspIleSerGluSerAlaLysAspPheIleCysHisLeuLeuGluLysAsp 261
                                                                                                       ValLeuAlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleThr 209
                                                                                                                        MetGluGlnAsnGlyIleMetSerThrAlaCysGlyThrProGlyTyrValAlaProGlu
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Patent No. 5856463
GENERAL INFORMATION:
APPLICANT: Prydz, Hans Peter Blankenborg
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TTCGAGACACACAGGAGCGGGTGTACATGGTGATGGAGCTGGAGGCCACGTGTTT
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          Disease
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150
72
123
59
                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,568A
FILING DATE:
                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz STREET: 600 South Avenue West
CITY: Westfield
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
          Uses
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Matches:
      TITLE OF INVENTION: PSKH-1 Ribozymes and TITLE OF INVENTION: Treatment NUMBER OF SEQUENCES: 14
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                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FOLGY, Shawn P.
REFERENCE/DÖCKET NUMBER: FOR:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
                                                                                                                                                                                                                                                                                                                        TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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664.50
54.958
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STRANDEDNESS: double
Brede,
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Best Local Similarity:
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GENERAL INCORNATION:
APPLICANT: UNTEN, Walter H.M.L.
APPLICANT: DARKER, Malter H.M.L.
APPLICANT: BARKER, Malter H.M.L.
APPLICANT: BASINA, Clare H.
APPLICANT: BLASINA, Alessandra
TITLE OF INVENTION: Human Checkpoint Kinase, hCDS1, Compositions and Methods
FILE REPERBNCE: TSRI 649.0
CURRENT APPLICATION NUMBER: US/09/529,093A
CURRENT FILING DATE: 1998-10-21
PRIOR FILING DATE: 1998-10-21
PRIOR FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 6
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                                                          GAGTACATTGCCCCAGAAGTCCTGGTCCGCAAGCCATACACCAACTCAGTGGACATGTGG
                                                                                                       SerIleGlyValIleThrTyrIleLeuLeuCysGlyTyrProProPheTyrGluGluThr
                                                                                                                        GluSerLysLeuPheGluLysIleLysGluGlyTyrTyrGluPheGluSerProPheTrp
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Patent No. 6413755
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Matches:
Conservative:
Mismatches:
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586.50
52.60%
36.98%
23.34%
2.0
SOFTWARE: Patentin Ver. SEQ ID NO 1
                                 TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                 ; NAME/KEY: CDS
; LOCATION: (66)..(1694)
US-09-529-093A-1
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Best Local Similarity:
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                      LENGTH: 1858
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DB:
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                                                                                     291 ValSerLeuGlnIleGlnLysAsnPheAlaLysSerLysTrpArgGlnAlaPheAsnAla 310
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US-09-746-694-3
Sequence 3, Application US/09746694
Fatent No. 6451538
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION:
FILE REFERENCE: RTS-0228
CURRENT APPLICATION NUMBER: US/09/746,694
CURRENT PRING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 49
FEWENCH: 1735
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Matches:
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                ValMetGlnLeuValSerGlyGlyGlyGluLeuPheAspArgIleLeuGluArgGlyValTyr 115
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                        LysHisGluAsnIleValThrLeuGluAspIleTyrGluSerThrThrHisTyrTyrLeu
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CURRENT APPLICATION NUMBER: US/09/800,960
CURRENT FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 4
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; Sequence 1, Application US/09800960
; Patent No. 6387677
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LENGTH: 2061
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                                                                                                                                                                                                                                                                     156
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36 193 54 253 74	94 373 114 433	134 493 154 553	171 613 191 670	211 730 231 790	251 850 271 910	291 970 310 103	33	36
ThrasnIleArgLysThrPheIlePheMetGluValLeuGlySerGlyAlaPheSerGlu [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	IleLysHisGluAsnIleValThrLeuGluAspIleTyrGluSerThrThrHisTyrTyr :::	TyrThrGluLysaspalaSerLeuValIleGlnGlnValLeuSeralaValLysTyrLeu	GluGluAsnSerLysIleMetIleThrAspPheGlyLeuSerLysMetGlu ::: ::: :: TGCAAGGGTGCCGCGTCAAGCTGGCTGATTTTGGCCTAGCCATCGAAGTACAGGGAGG GlnAsnGlyIleMetSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu	AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleThrTyrIle ::		LeuSerHisProTrplleAspGlyAsnThrAlaLeuHisArgAspIleTyrProSerVal ::	AlaalayalyalHisHisMetArgLysLeuHisMetAsnLeuHisSerProGlyValArg ACCATGCTTGTCTCCAGGAACTTCTCAGTTGGCAGGCAGG	GTCGGATG
17 134 37 194 55	75 314 95 374	115 434 135 494	155 554 172 614	192 671 212 731	232 791 252 851	272 911 292 971	311 1031 331	347
	oy og	oy oy	67 da 69	00 Qd	oy da	& qa & qa	do do	2 6 G

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1206 AAACCACTGTGGTACACACACGCTACAGATGGGATCAAGGGCTCCACAGAGAGCTGCAACA 1265
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                                                                                                                                                    384 ProGlyGlyArgSerLeuAsnCysLeuValAsnGlySerLeuHisIleSerSerLeu 403
                                                                                                                              404 ValProMetHisGlnGlySerLeuAlaAlaGlyProCysGlyCysCysSerSerCysLeu 423
                                                                                                                                                                                             ---SerTyrCysSerGluProThrLeu 439
364 SerValAlaLeuProAlaLeuThrGlnLeuProCysGlnHisGlyArgArgProThrAla 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: CURRESSEE: CURRESSEE: CURRESSEE: CURRESSEE: 1420 Fifth Ave., Suite 2800
STREET: 1420 Fifth Ave., Suite 2800
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101-2347
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIR RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2934
                                                                                                                                                                                                                                                                                                                        1389 CTCTCTGCTCCTCAGCCATGCGAAAACAGGAGATCA 1424
                                                                                                                                                                                                                                                          440 LeuLysLysAlaAsnLysLysGlnAsnPheLysSer 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/198,446B
FILING DATE: 18-FEB-1994
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FHCR17537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: FHCR.
TELECHONE: 206-82-8100
TELEPHONE: 206-82-8100
TELEFAX: 206-224-0779
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
LENGTH: 2934 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA to mRNA DESCRIPTION: yeast MEC2 CDNA
                                                                                                                                                                                              424 AsnileGlySerLysGlyLysSer--
                                                                                                1266 CCACCACAGAAG-------
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TOPOLOGY: lin
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US-08-198-446B-16
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Pred. No.:
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Score: Percent Best Lo Query N	e: ent Si Local y Mato	ore: rcent Similarity: st Local Similarity: ery Match:	562.50 48.50% 33.55% 22.38%	Matches: Conservative: Mismatches: Indels: Gaps:	157 70 165 78 15	
us-0	096-6	-643-2 (1-476)	x US-08-198-44	6B-16 (1-2934)		
Qy Dp	10	SerSerTrpLysL CATCAATGGTGG	SerSerTrpLysLysGlnThrThrAsnIleArgLysThrPheIlePheMetGluVa. 	eargLysThrPhe 	c3 — t5	28 1003
Oy Dp	29	LeuGlySerGlyA ::: GrGGGCCAGGGTG	laPheSerGluValPh ::: CATTTGCCACAGTAAA	neLeuValLysGlnAr ::: NGAAAGCCATTGAAAG	LeuGlySerGlyAlaPheSerGluValPheLeuValLysGlnArgLeuThrGlyLysLeu :::	48
ογ	49	PheAlaLeuLysC	.ysileLysLysSerPr	coalaPheArgAsp		67
g	1064	TTCGCGGTGAAGA	TTATAAGTAAACGCAA	AGTAATAGGCAATAT	GGATGGTGTGACAAGA	1123
Qy Dp	68 1124	GlulleAlaValL ::: GAGTTAGAAGTAT	euLysLysIleLysHi { ::: :: TGCAAAAGCTCAATCP	SGluAsnIleValTh 	GlullealavalLeuLysLyslleLysHisGluasnIleValThrLeuGluaspileTyr ::: :: :: GGGTTAGAAGTATGCAAAAGCTCAATCCAAGGATAGTACGATTGAAAGGATTTTAT	87 1183
Qy Dp	1184	GluSerThrThrH GAAGATACTGAGA	:\sTyrTyrLeuValMe :GTTATATATGGTGAI	etGlnLeuValSerGl ::: GGAGTTCGTTTCTGG	GluSerThrThrHisTyrTyrLeuValMetGlnLeuValSerGlyGlyGluLeuPheAsp 	107 1243
οy	108		glleLeuGluArgGlyValTyrThrGluLysAspAlaSerLeuValIl	uLysAspAlaSerLe	uValIleGlnGlnVal	127
qq	1244	::: TTTGTTGCTGCTC	::: :: ::: ::: ::: :: ::: :: ::: :: ::: :: :::	 AGATGCTGGGAGGGA	∡	1303
Qy	128		ysTyrLeuHisGluAs ::: AATACATTCACTCTAT	snGlyIleValHisAr GGGCATCAGCCATCG	LeuSeralaValLysTyrLeuHisGluasnGlyIleValHisArgAspLeuLysProGlu ::: :: ::: CTCACAGCAATAAAATACATTCACTCTATGGGCATCAGCCATCGTGACCTAAAGCCCGAT	147 1363
Oy Dp	148	AsnLeuLeuTyrL ::: AATATTCTTA	euThrProGluGluAs :: :::: :TGAACAAGACGATCC	nSerLysIleMetIl ::: :TGTATTGGTAAAGAT	AsnLeuLeuTyrLeuThrProGluGluAsnSerLysIleMetIleThrAspPheGlyLeu :::	167 1420
oy G	168	SerLysMetGluG	lnasnGlyIleMe GAAATGGGTCTTTAT	stSerThrAlaCysGl	SerLysMetGluGlnAsnGlyIleMetSerThrAlaCysGlyThrProGlyTyrVal ::: ::::: GDAAAGTACAAGGAATGGGTCTTTTATGAAAACTTCTGGGCATTTGCATATGG	186 1480
ò	187	AlaProGluValL	euAlaGlnLvs			4
7 d	1481	GCACCTGAAGTCA	::	ATCCGTATCTCCTGA		r ici
Qy	195 1541	ProTyrSerL AATGAGTACTCTF	ysalavalaspCysTr CGTTAGTGGATATGTQ	rpSerIleGlyValIl :: GTCAATGGGATGTCT	ProTyrSerLysAlaValAspCySTrpSerIleGlyValIleThrTyrIleLeuLeu 	213 1600
δ i	214	CysGlyTyrProP	roPheTyrGluGluTh	rGluSerLysLeuPh	CysGlyTyrProProPheTyrGluGluThrGluSerLysLeuPheGluLysIleLysGlu	33
g	0	ACGGGCCACTTAC	CTTTTAGTGGTAGCAC	CACAGGACCAATTATA	TAAACAGATTGGAAGA	ف
Qy Dp	234	GlyTyrTyrGluP GCTCATATCAT-	GlyTyrTyrGluPheGluSerProPheTrpasp- 	rpaspaspilese AGATTTCCGGATATC	heGluSerProPheTrpAspAspIleSerGluSerAlaLysAsp 	252 1717
Qy Dp	253	PhelleCysHisL TTCATAGATTCAT	euLeuGluLysAspPr TGTTACAGGTGGATCC	coAsnGluArgTyrTh AAATAATAGGTCGAC	PhelleCysHisLeuLeuGluLysAspProAsnGluArgTyrThrCysGluLysAlaLeu 	272 1777
oy d	273	SerHisProTrpI	leAspGlyAsnThrAl	la-LeuHisArg	SerHisProTrpIleAspGlyAsnThrAla-LeuHisArg	285
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1898 TACGAATTTGTCAAAGCCCAAAGGAAATTACAAATGGAGCAACAACTTCAAG----- 1949
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                                                                                               -----AACAGGATCAGGAAGACCAAGATGGAAAAATTCAAGGATTTAAAATACCCGCA 2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: USA7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elb FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,693
FILING DATE: February 18, 1994
APPLICATION NUMBER: DCT/US93/04456
FILING DATE: February 18, 1994
APPLICATION NUMBER: DCT/US93/04456
FILING DATE: May 12, 1993
APPLICATION NUMBER: US 07/884,426
FILING DATE: May 14, 1992
APPLICATION NUMBER: US 07/882,051
FILING DATE: May 12, 1993
APPLICATION NUMBER: US 07/882,051
FILING DATE: May 12, 1992
ATION DATE: May 12, 1992
ATIONERY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Hartwell, Leland H.
APPLICANT: Weinert, Ted A.
APPLICANT: Plon, Sharon E.
APPLICANT: Plon, Sharon E.
APPLICANT: INVENTION: Cell Cycle Checkpoint Genes
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                       aValValHisHisMetArgLysLeuHisMet------
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REGISTRATION NUMBER: 35,356
REFENCE/COKET NUMBER: FHCR110798
TELECOMMUNICATION:
TELEPHONE: 206-682-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/08870693
Patent No. 5866338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2284 -----TGCTGT 2289
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312 aValValHisHisMetArgLysLeuHisMet----
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PRIOR FILING DATE: 1996-03-12
NUMBER OF SEC ID NOS: 4
SOFTWARE: PASTSEC FOR WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1, Application US/09142551A; Patent No. 6218136
| Patent No. 6218136
| GENERAL INFORMATION:
| APPLICANT: KUMAR, SANJAY
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US-09-142-551A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                           LeuGlySerGlyAlaPheSerGluValPheLeuValLysGlnArgLeuThrGlyLysLeu 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerSerTrpLysLysGlnThrThrAsnIleArgLysThrPhe----IlePheMetGluVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PheAlaLeuLysCysIleLysLysSerProAlaPheArgAsp---SerSerLeuGluAsn
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1157
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                           ORGANISM: Saccharomyces cerevisiae
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TELEFAX: 206-224-0779
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
LENGTH: 2934 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
DESCRIPTION: yeast MEC2 CDNA
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562.50
48.50%
33.55%
22.38%
                                                                                                                                                                                    CDS
395..2724
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Best Local Similarity:
                                                                                                                                 ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                      HYPOTHETICAL:
                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                         Alignment Scores:
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                                                                                                                                                                         FEATURE
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                                                                                                                                                                                                                  PhelleCysHisLeuLeuGluLysAspProAsnGluArgTyrThrCysGluLysAlaLeu 272
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APPLICANT: LIVI, GEORGE P.
APPLICANT: MCLAUGHLIN, MEGAN M.
APPLICANT: MCLAUGHLIN, MEGAN M.
APPLICANT: MCLAUGHLIN, METHODS OF THE IDENTIFICATION OF
TITLE OF INVENTION: PHARMACEUTICALLY ACTIVE COMPOUNDS
FILE REPERENCE: P50448
CURRENT APPLICATION NUMBER: US/09/142,551A
CURRENT APPLICATION NUMBER: PCT/US9//04256
PRIOR FILING DATE: 1999-09-10
                                                                                                                                                                                                                                                                                                                                                     273 SerHisProTrplleAspGlyAsnThrAla-LeuHisArg---
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ORGANISM: Homo sapiens
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US-09-159-385-3
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ATTGTCTGCATCCTGGATGTGTATGAGAACATGCACCATGGCAAGCGCTGTCTCCTCATC 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 ProGluGluAsnSerLysIleMetIleThrAspPheGlyLeuSerLysMetGluGlnAsn 173
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Conservative:
Mismatches:
Indels:
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                                                                                      Length:
                                                                               3.46e-43
542.50
52.02%
34.09%
21.59%
ORGANISM: Homo sapiens
                                                                                                                Percent Similarity:
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                      US-09-142-551A-1
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                                         GACGAAGTCAAGGAGGAGATGACCAGTGCCCACTATGCGGGTAGACTACGA-----
                                                                                     HisSerProGlyValArg-ProGluValGluAsnArgProProGluThrGlnAlaSer--
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APPLICANT: KAWAI, TARO
TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
FILE REFERENCE: P4-569
CURRENT APPLICATION NUMBER: US/09/159,385
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: JP97/261589
BARLIER FILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3:
LENGTH: 2132
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                         GENERAL INFORMATION:
APPLICANT: AKTRA, SHIZUO
APPLICANT: KAWAI, TARO
TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
FILE REFERENCE: 081356/0128
CURRENT APPLICATION NUMBER: US/09/186,277
CURRENT FILING DATE: 1999-11-05
EARLIER APPLICATION NUMBER: JP97/261589
EARLIER PILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3
LENGTH: 2132
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Mismatches:
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Matches:
Sequence 3, Application US/09186277 Patent No. 6171841
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21.59%
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US-09-186-277-3
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Best Local Similarity:
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682 GAGGCGGACATGTGGAGCATCGGTGTCATCACCTATATCCTCCTGAGCGGTGCATCCCCG 741
                               PheTyrGluGluThrGluSerLysLeuPheGluLysIleLysGluGlyTyrGluPhe
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CORRESPONDENCE Akzo No. 5614195el Patent Department
STREET: 1300 Piccard Drive, Suite 206
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Fatent No. 5614195
GENERAL INFORMATION:
APPLICANT: Tomley, Fiona M.
APPLICANT: Bunnstead, Janene M.
APPLICANT: Wermeulen, Arno N.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 10
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CITY: Rockville
STATE: Maryland
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49 ACAGCACAGGAATATGCAGTAAAAGTAATATCTAAACGTCAAGTAAAACAGAAGACAGAT 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuValIleGlnGlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIleValHis 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuGlu------AsnGluIleAlaValLeuLySLySIleLySHisGluAsnIleVal 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGTATAGTACGTCAGGTTCTATCGGGTATAAATTATATATGCATCGTAATAAAATAGATCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
CLONE: Em70-1
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                         APPLICATION NUMBER: US/08/464,164 FILING DATE: June 2, 1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE: sporozoite IMMEDIATE SOURCE:
                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.14e-42
537.50
57.70%
40.00%
21.39%
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eimeria maxima
                                                                                                                                                                                                                                                                      LENGTH: 1400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN: Houghton
                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-464-164-1
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199 PheAlaLysSerLysTrpArgGlnAlaPheAsnAlaAlaAlaValValHisHisMetArg 318
162 IleThrAspPheGlyLeuSer---LysMetGluGlnAsnGlyIleMetSerThrAlaCys 180
                                                                                                                                                                                                                                              GGAGCAAATGAATTTGAAATTCTAAAGAAAGTCGAGAAAGGAAAATTCACCTTCGATTTA 645
                                                                                                                                                                                                                                                                               241 ProPheTrpAspAspIleSerGluSerAlaLysAspPheIleCysHisLeuLeuGluLys 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AspCysTrpSerIleGlyValIleThrTyrIleLeuLeuCysGlyTyrProProPheTyr
                                                                                                                                                        261 AspProAsnGluArgTyrThrCysGluLysAlaLeuSerHisProTrpIleAspGlyAsn
                                                                                                                                                                                                                                                                                                                                                                                                                       281 ThrAlaLeuHisArgAspIle----TyrProSerValSerLeuGlnIleGlnLysAsn
                                                                                                                                                                                                        GluGluThrGluSerLysLeuPheGluLysIleLysGluGlyTyrTyrGluPheGluSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tomley, Fiona M.
APPLICANT: Dunn, Paul P. J.
APPLICANT: Bunstead, Janene M.
APPLICANT: Vermeulen, Arno N.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Organon Teknika Corporation
STREET: 1330 Piccard Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93.309078.9
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08338057
Patent No. 5795741
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Gormley, Mary E. REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
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STATE: Maryland
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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82 ThrLeuGluAspileTyrGluSerThrThrHisTyrTyrLeuValMetGlnLeuValSer 101
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                     Length:
                                                                                                                     ORGANISM: Eimeria maxima
STRAIN: Houghton
DEVELOPMENTAL STAGE: sporozoite
                                                     MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                   1.14e-42
537.50
57.70%
40.00%
21.39%
LENGIH: 1400 base pairs
                                                                                            FRAGMENT TYPE: C-terminal
        TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                               1..1368
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Query Match:
                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                          ORIGINAL SOURCE:
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                                                                    HYPOTHETICAL:
ANTI-SENSE: N
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                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                               ; LOCATION:
US-08-338-057-1
                                                                                                                                                                            LIBRARY:
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                     GATGTTACTGCTAAGGATAGTATTAATCTTCCTTCTTGAGAGTACTATA---CTTAAT 822
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ProPheTrpAspAspIleSerGluSerAlaLysAspPheIleCysHisLeuLeuGluLys 260
                                                                                                              706 GTACCCTCAATGCGTATATCAGCAAAAGATGCATTAGATCATCCATGGATAAAAAGTACA 765
                                                                                                                                                   281 ThralaLeuHisArgAspIle-----TyrProSerValSerLeuGlnIleGlnLysAsn 298
                                                                            AspProAsnGluArgTyrThrCysGluLysAlaLeuSerHisProTrpIleAspGlyAsn
                                                                                                                                                                                                                            PheAlaLysSerLysTrpArgGlnAlaPheAsnAlaAlaAlaValValHisHisMetArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: TELOPPY disk

COMPUTER: TELOPPY disk

COMPUTER: TBM PC compatible

CONFINENT APPLICATION DATA:

APPLICATION NUMBER: US/08/66,416

FILING APPLICATION:

PRIOR APPLICATION THE NUMBER: US/08/464,164

FILING APPLICATION INFORMATION:

NAME: GOTTAL NUMBER: 34,409

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION TO SEG 1D NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1400 base pairs

TYPE: DIACLE: CANDA COMPANION:

TYPE: DIACLE: CANDA COMPANION:

TYPE: TINCARIA CALIBRATION:

TYPE: TINCARIA CALIBRATICS:

LENGTH: 1400 base pairs

TYPE: TINCARIA CALIBRATICS:

LENGTH: 110 AND CALIBRATICS:

TOTOCLOGY: LINEAT

TOTOCLOGY: LINEAT

TOTOCLOGY: LINEAT

TOTOCLOGY: LINEAT
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Sequence 1, Application US/08668416
Patent No. 584372.
Sequence 1, Application US/08668416
Patent No. 584372.
Patent No. 584372.
Patent No. 584372.
Patent Norman No. Application M.
APPLICANT: Dunn, Paul P. J.
APPLICANT: Bunatead, Janene M.
APPLICANT: Vermeulen, Arno N.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
CLONE: Em70-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Akzo No. 5843722el Patent Department STREET: 1300 Piccard Drive, Suite 206 CITY: Rockville STATE: Rockville COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN: Houghton
DEVELOPMENTAL STAGE: sporozoite
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                                                                                                                                                                                                                                                                                                                                       883 AAATTAACAACAAAT 897
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GlyThrProGlyTyrValAlaProGluValLeuAlaGlnLysProTyrSerLysAlaVal 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 ArgAspLeuLysProGluAsnLeuLeuTyrLeuThrProGluGluAsnSerLysIleMet 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09 AAAGAATTATTAATAAAGAAGTTGAATTATTAAAGAAATTAGATCATCCTAATATCATG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                   82 ThrieuGluAspileTyrGluSerThrThrHisTyrTyrLeuValMetGlnLeuValSer 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 GlyGlyGluLeuPheAspArgIleLeuGluArgGlyValTyrThrGluLysAspAlaSer 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 LeuValIleGlnGlnValLeuSerAlaValLysTyrLeuHisGluAsnGlyIleValHis 141
                                                                                                                                                                                                                                    241 ProPheTrpAspAspIleSerGluSerAlaLysAspPheIleCysHisLeuLeuGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 AspProAsnGluArgTyrThrCysGluLysAlaLeuSerHisProTrplleAspGlyAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 AAATTATATGAATTCTTTGAGGATAAAGGATACTTTTATCTTGTTACAGAAGTATATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IleThrAspPheGlyLeuSer---LysMetGluGlnAsnGlyIleMetSerThrAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 AspCysTrpSerIleGlyValIleThrTyrIleLeuLeuCysGlyTyrProProPheTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 GluGluThrGluSerLysLeuPheGluLysIleLysGluGlyTyrTyrGluPheGluSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281 ThralaLeuHisArgAspIle-----TyrProSerValSerLeuGlnIleGlnLysAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 ThrGlyLysLeuPheAlaLeuLysCysIleLysLysSerProAlaPheArgAspSerSer
                                                                                                                                                                                                                                                                                                                                                                         65 LeuGlu------AsnGluIleAlaValLeuLysLysIleLysHisGluAsnIleVal
                                                                                 1400
122
54
116
13
                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                        US-09-960-643-2 (1-476) x US-08-668-416-1 (1-1400)
                                                                                                      Matches:
                                                                                      Length:
                                                                            1.14e-42
537.50
57.70%
40.00%
21.39%
                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                      Alignment Scores:
; NAME/KEY:
; LOCATION:
US-08-668-416-1
                                                                                                                                                    Query Match:
                                                                                      Мо.:
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823 ATCAGGCAGTICCAGGGTACACAGAAGCTTGCTGCTGCTGCTGCTGTTACATGGGGAGT 882 qq

319 LysLeuHisMetAsn 323 ||||||| 883 AAATTAACAACAAT 897

οy q

Search completed: March 15, 2003, 07:51:43 Job time : 79 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

March 14, 2003, 14:04:21 ; Search time 14 Seconds (without alignments) 1410.195 Million cell updates/sec

US-09-960-643-2

2513 1 MGRKEEDDCSSWKKQTINIR.....VKASGSSHCRAGQTGVCLIM 476 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q63450 rattus norv	Q14012 homo sapien	mus m	P25323 dictyosteli	P13234 rattus norv		Q00771 emericella	P11801 homo sapien		O15075 homo sapien	.09jlm8 mus muscalu	Q13554 homo sapien	rattu	Q9uqm7 homo sapien		Q9z265 mus musculu	Q13557 homo sapien		P22517 saccharomyc	P11798 mus musculu	P28652 mus musculu	rattı	homo		sacc	Q923t9 mus musculu	P11730 rattus norv	O14408 metarhizium	_	0.0	P28583 glycine max	22	22
SUMMARIES	ΩI	KCC1_RAT	KCC1_HUMAN	KCC4_MOUSE	KMLC_DICDI	KCC4_RAT	KCC4_HUMAN	KCC1_EMENI	KPSH_HUMAN	KCC1_SCHPO	DCK1_HUMAN	DCK1_MOUSE	KCCB_HUMAN	DCK1_RAT	KCCA_HUMAN	KCCA_RAT	CHK2_MOUSE	KCCD_HUMAN	KCCD_RAT	KCC2_YEAST	KCCA_MOUSE	KCCB_MOUSE	KCCB_RAT	CHK2_HUMAN	KCCG_HUMAN	KCC1_YEAST	KCCG_MOUSE	KCCG_RAT	KCC1_METAN	SPK1_YEAST	CDP1_ARATH	CDPK_SOYBN	DAPK_HUMAN	RCK1_YEAST
	Length DB	374	370 1													478 1	546 1					542 1												512 1
96	Query Match Le	0.	45.9	27.8	27.6	27.6	27.2	25.9	25.6	25.1	24.4	24.1	24.0	24.0	24.0	23.8	23.8	23.7	23.5	23.4	23.2	23.1	23.0	23.0	23.0	23.0	22.8	22.5	22.5	22.2	22.1	•	21.6	21.3
	Score	10	1152.5	697.5	694.5	692.5	684	651	643.5	630	612	909	603.5	602.5	602	599	297	594.5	591.5	588	584	579.5	578.5	578.5	578	577.5	27	. 99	565.5	22	56.	÷.	43.	3
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EMBL; L24907; AAA19670.1; -. EMBL; L26288; AAA66944.1; -. PDB; 1A06; 08-APR-98.

P53683 oryza sativ										
CDP2_ORYSA	NOAL_HUMAN	KAA1 RAT	KMLS_RABIT	CDP2_MAIZE	K6A1_MOUSE	CDP3_ORYSA	KMLS_CHICK	DUN1_YEAST	KMLS_HUMAN	CDP1_ORYSA
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21.3 533	_	7	_				_			
	21.1	21.1	21.1	21.1	21.0	21.0	20.9	20.8	20.7	20.7

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                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (42 KDA ISOFORM).
STRAIN=Sprague-Dawley; TISSUE=Lung;
MEDLINE=95035115; Pubmed-1948038;
Cho F.S., Phillips K.S., Boucki B., Weaver T.E.;
"Characterization of a rat cDNA clone encoding calcium/calmodulin-dependent protein kinase I.";
Biochim. Biophys. Acta 1224:156-160(1994).
                                                            KCCI_RAT STANDARD; PRT; 374 AA.
063450; 063084;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAX-2000 (Rel. 39, Last annotation update)
Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)
(CAM kinase I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (37 KDA ISOFORM).
MEDLINE-94075341; Pubmed=8253780;
Picciotto M.R., Czernik A.J., Nairn A.C.;
"Calcium/calmodulin-dependent protein kinase I. cDNA cloning and identification of autophosphorylation site.";
J. Biol. Chem. 268:26512-26521(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF SHORT FORM TISSUE=Brain; MEDLINE=96182648; PubMed=8601311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
RESULT 1
                                                                        HID DESCRIPTION OF COLOR COLOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 VLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 VKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMSTACGTPGYVAPE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 VLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISES 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 AKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 AAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAPVLDHSVALPA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTQLPCQHGRRPTAPGGRSLNCLVNGSLHISSSLVPMHQGSLAAGPCGCCSSCLNIGSKG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 WKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPAFRDSSLENEIA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; lervouss; 1.

Promos; primase; 1.

Probos; primase; 1.

Probos; profolo; Ext.pkinase; 1.

SMART; SM00220; S_TKc; 1.

PROSITE; PS00108; PROTEIN KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN KINASE_BOM; 1.

PROSITE; PS50011; PROTEIN KINASE_BOM; 1.

Transferase; Serine/Chreonine-protein kinase; Calmodulin-binding; Phosphorylation; ATP-binding; Alternative splicing.

Phosphorylation; ATP-binding; Alternative splicing.
                                                                                                                                                              SUBUNIT: MONOMER.
ISSUE SPECIFICITY: UBIQUITOUS.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CAMK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
PHOSPHORYLATION (AUTO-).
K->A: LOSS OF ACTIVITY.
57FA20ECE00FA76C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 2e-65; 46; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.9%; Score 1152.5;
55.8%; Pred. No. 2e-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nic, DiterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41337 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L41816; AAA99458.1; -. HSSP; Q63450; 1A06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:1459; CAMK1.
MIM; 604998;
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49
141
177
49
370 AA;
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BINDING
ACT_SITE
MOD_RES
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                                                                                                           R PROSITE; PSOU107; PROTEIN_KINASE_ATP; 1.

R PROSITE; PSOU108; PROTEIN_KINASE_ATP; 1.

R PROSITE; PSOU108; PROTEIN_KINASE_ST; 1.

PROSITE; PSOU108; PROTEIN_KINASE_DOM; 1.

Transferase; Serine/threonine-protein kinase; Calmodulin-binding;

M Transferase; Serine/threonine-protein kinase; Calmodulin-binding;

T POMAIN 20 276 PROTEIN KINASE.

T POMAIN 287 321 ATP (BY SIMILARITY).

T PACT_SITE 141 141 BY SIMILARITY).

T ACT_SITE 141 141 BY SIMILARITY).

T ACT_SITE 141 147 PHOSPHORYLATION (AUTO-).

T SAPPPESGAQMASHGELLIPPRAGGPARGCCCRDCCVEPGSELP
T VARSPLIC 323 374 FORDEN. CONTROLLIPPRAGGPARGCCCRDCCVEPGSELP
T PACT_SITE 141 187 PHOSPHORYLATION (AUTO-).

T SAPPPESGAQMASHGELLIPPRAGGPARGCCCRDCCVEPGSELP
T SOUNTS 110 110 PHOSPHORYLATION (AUTO-).

T SAPPPESGAD. - HOPGGTGTDS (IN 37 KDA ISON).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 VKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMSTACGTPGYVAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 VLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 AKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFN
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type I (EC 2.7.1.123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                F -> G (IN REF. 1).
A -> R (IN REF. 1).
A -> R (IN REF. 1).
; 37889B3DEF033AB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.0%; Score 1155.5; DB 69.6%; Pred. No. 1.3e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Calcium/calmodulin-dependent protein kinase t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 AA.
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
ProCom; PD000001; Euk_pkinase; 1.
SWART; SW00220; S_TKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41638 MW;
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| ATAVVRHMRKLQLGTSQEG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 222; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Q14012;
                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
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KCC1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309
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Tan J.L., Spudich J.A.;
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KMLC_DICDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Nati. Acad. Sci. U.S.A. 84:3038-3042(1987).
-!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
-!- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL
                                                                                                                                                                                                                                  P08414; 061381; 01-301. Created) 01-AUG-1988 (Rel. 08, Created) 01-APR-1993 (Rel. 25, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Calcium/calmodulin-dependent protein kinase type IV catalytic chain (EC 2.7.1.123) (CAM kinase-GR) (CAMK IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Screening an expression library with a ligand probe: isolation and sequence of a cDNA corresponding to a brain calmodulin-binding
------AAG-C-CCRDC-----
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- TISSUE SPECIFICITY: BRAIN AND TESTIS.
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CAMK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hahn W.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BALB/C; TISSUE-Brain;
MEDLINE=91372388; PubMed=1893997;
Jones D.A., Glod J., Wilson-Shaw D., Hahn W.E., Sikela J.M.;
"CDNA sequence and differential expression of the mouse
Ca2+/calmodulin-dependent protein kinase IV gene.";
FEBS Lett. 289:105-109(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89122027; PubMed-2536634; Sikela J.M., Taw M.L., Rao F.-T., Hartz J.A., Wel Q., Sikela J.M., Taw M.L., Rao F.-T., Hartz J.A., Wel Q., "Chromosomal localization of the human gene for brain Ca2+/calmodulin-dependent protein kinase type IV.";
                                                                                                                                                                                                                   469 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam, PF00069; pkinase; 1.
ProDom; PD0000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
    ----QEGQGQTASHGELLTPVAGGP---
                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
MEDLINE=87204263; PubMed=3033675;
Sikela J.M., Hahn W.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 315-469 FROM N.A.
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SEQUENCE OF 240-469 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M16206; AAA39933.1; -. EMBL; M64266; AAA37364.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J03057; AAA37366.1; -. X58995; CAA41741.1; -.
                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics 4:21-27(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A29878; A29878.
PIR; S17656; S17656.
HSSP; Q63450; 1A06.
MGD; MGI:88258; Camk4.
                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                 430 KSSYCSEP 437
                                                                                               ----CVEP 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                KCC4 MOUSE
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EMBL;
                                                                                                                                                                                                                                                                                                                                                                                   CAMK4
    325
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174 GIMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEET-ESKLFEKIK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 EGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTA--LHRDIYPS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 NCEYYFISPWMDEVSLNAKDLVKKLIVLDPKKRLITFQALQHPWVTGKAANFVHMD--T 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSK-MEQN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKSPAFRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGV 114
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                               9 CSSWKKQTTNIRKTF-----IFMEV---LGSGAFSEVFLVKQRLTGKLFALKCI 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tan J.L., Spudich J.A.; "Characterization of the Dictyostelium myosin light chain kinase cDNA. Identification of an autoinhibitory domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 VSLQIQKNFAKSKWRQAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETS 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309 AQKKLQEFNARRKLKAAVKAVVASSRLGSASSSHTSIQENHKASSDPPSTQDAKDS 364
                                                                                                                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                         DB 1; Length 469;
                                                                                                                    ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
CALMODULIN-BINDING (POTENTIAL).
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS001108; PROTEIN_KINASE_AT; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                       Score 697.5; DB 1; Length 4; Pred. No. 8.6e-37; 60; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spudich J.A.; Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                          VLD -> CFGI (IN REF. 2).
N -> T (IN REF. 2).
CE1F98670822F975 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
NCBL_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1992 (Rel. 22, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Myosin light chain kinase (EC 2.7.1.117) (MLCK).
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                                                                                                       PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 266:16044-16049(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91340753; PubMed=1651931;
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MEDLINE=90337997; PubMed=2380188;
                                                                                                                                                                                                                                                   MW
                                                                                                                                                                                                                                                                                         27.8%;
                                                                                                296
56
71
160
337
280
302
                                                                                                                                                                                                                                                                                                               Best_Local Similarity 42.7
Matches 152; Conservative
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                                                                                                                                                                                    318
278
302
469 AA;
                                                                                 Calmodulin-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARTIAL SEQUENCE.
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                                                                                                                                                                 ACT_SITE
DOMAIN
                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                        NP_BIND
BINDING
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                                                                                                       DOMAIN
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gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 HENGIVHRDLKPENLLYLTPEENSKIMITDFGLSK-MEONGIMSTACGTPGYVAPEVLAO 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 KPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDF 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 IKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRD--SSLENEIAVLKK 74
                                J. Biol. Chem. 265:13818-13824(1990).
                                                                       MYOSIN LIGHT CHAIN.
-!-CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin light-chain] phosphate.
-!- ENZYME REGULATION: POSSESSES AN AUTOINHIBITORY DOMAIN.
--- AUTOHOSPHORYALATION APPEARS TO INCREASE THE ENZYMATIC ACTIVITY.
DOES NOT HAVE A CALADODLIN-BINDING DOMAIN.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
"Dictyostelium myosin light chain kinase. Purification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / SIMILARITY.
546CAEED8F6ECD0B CRC64;
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AUTOINHIBITORY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP (BY SIMILARITY). ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.6%; Scor.
50.2%; Pred. No. /...
52; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, Q63450; 1A06.
DictyDb; DD01034; mlkA.
InterPro: IPR000719; Eul_pkinase.
InterPro: IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM0220; S.TKC; 1.
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P13234;
01-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33406 MW;
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M64176; AAB06337.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265
295
22
37
                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A40811; A40811.
PIR; A37125; A37125.
                                                                                                                                                                                                                   CAMK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00107;
                    characterization
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SEQUENCE
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BINDING
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KCC4_RAT
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-i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CAMK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- ALTERNATIVE PRODUCTS: 2 isoforms; 1/calcium-calmodulin-dependent protein kinase type IV catalytic chain (shown here) and 2/calspermin; are produced by alternative splicing.
01-APR-1993 (Rel. 25, Last sequence update)
L-UN-2002 (Rel. 41, Last annotation update)
Calcium/calmodulin-dependent protein kinase type IV catalytic chain
(EC_2.7.1.123) (CAM kinase-GR) (CaMK IV) (Calspermin).
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MEDILNE-96094352; PubMed-7493991;
Sun Z., Means R.L., LeMagueresse B., Means A.R.;
"Organization and analysis of the complete rat calmodulin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A novel Ca2+/calmodulin-dependent protein kinase and a male germ cell-specific calmodulin-binding protein are derived from the same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 306-474 FROM N.A. (ISOFORM 2), AND SEQUENCE OF 335-361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: CAM KINASE GR IS A NEURONAL-SPECIFIC PROTEIN KINASE, ENRICHED IN CEREBELLAR GRANULE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Sprague-Dawley;
MEDLINE=89123272; PubMed=2914893;
Ono T., Slaughter G.R., Cook R.G., Means A.R.;
"Molecular cloning sequence and distribution of rat calspermin, a high affinity calmodulin-binding protein.";
J. Biol. Chem. 264:2081-2087(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohmstede C.-A., Bland M.M., Merrill B.M., Sahyoun N., Relationship of genes encoding Ca2+/Calmodulin-dependent protein kinase Gr and calspermin: a gene within a gene."; Proc. Natl. Acad. Sci. U.S.A. 88:5784-5788(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohmstede C.-A., Jenson K.F., Sahyoun N.;
"Ca2+/calmodulin-dependent protein kinase enriched in cerebellar granule cells. Identification of a novel neuronal calmodulin-dependent protein kinase.";
J. Biol. Chem. 264:5866-5875(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISOFORMS 1 AND 2), AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Means A.R., Cruzalegui F., Lemagueresse B., Needleman D.S., Slaughter G.R., Ono T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is testis-specific.
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STRAIN-Sprague-Dawley; TISSUE-Brain;
MEDLINE-89174647; PubMed=2538431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
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J. Biol. Chem. 270:29507-29514(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1 AN)
MEDLINE-91288548; Pubmed-1648230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91304387; PubMed=1649385;
                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
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Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                  Biochem. 115:637-640(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virol. 68:1697-1705(1994).
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HSSP; Q63450; 1A06.
Genew; HGNC:1464; CAMK4.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 142:191-197(1994).
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60
75
         Eukaryota; Metazoa;
                           Mammalia; Eutheria;
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                   SEQUENCE FROM N.A.
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52
75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Blood;
                                                                                                                                                                                                 kinase IV.
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NP_BIND
BINDING
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         10;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
calcium/calmodulin-dependent protein kinase type IV catalytic chain (EC 2.7.1.123) (CAM kinase-GR) (CAMK IV).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
CALMODULIN-BINDING (POTENTIAL).
POLY-GLU.
                                                                                                                                                                                                                              PROBLEM PRINCES OF STATES 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62; Mismatches 120; Indels
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I -> M (IN REF. 2 AND 4).

56F71AC5644DED23 CRC64;
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InterPro; IPR002290; Ser_thr_pkinase.
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AAA40845.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
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                                               EMBL; M64757; AAA40856.1; --
EMBL; M64757; AAA40857.1; --
EMBL; J046600; AAA41867.1; --
EMBL; J04446; AAA40900.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      56
71
160
337
399
                                                                                                                                             PIR; A41103; TVRTC4.
HSSP; Q63450; 1A06.
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71
160
318
393
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  M63334; M74488;
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Q16566;
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BINDING
ACT_SITE
DOMAIN
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    DRAMA KAMAMANA SALAHAN SALAHAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN.
-!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
-!- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL
-!- SUBCELLULAR (BY SIMILARITY).
-!- ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE
-!- ALTERNATIVE CHAIN AND CALSPERMIN ARE OBTAINED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94149862; PubMed-8107230;
Mostalos G., Hanissian S.H., Jawahar S., Vara L., Kieff E.,
Chatila T.A.;
"A Ca2+/calmodulin-dependent protein Kinase, CaM Kinase-Gr, expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       after transformation of primary human B lymphocytes by Epstein-Barr virus (EBV) is induced by the EBV oncogene LMP1.";
MEDLINE-94375404; PubMed-8089075;
Kitani T., Okuno S., Fujisawa H.;
"CDNA cloning and expression of human calmodulin-dependent protein
                                                                                                                                                                                                                                                                                  TISSUE-Cerebellum, and Thymus;
MEDLINE-94255566; PubMed-8194751;
Bland M.M., Monroe R.S., Ohmstede C.A.;
"The cDNA sequence and characterization of the
Ca2+/calmodulin-dependent protein kinase-Gr from human brain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CAMK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00069; pkinase; 1. Probom; PP000001; Euk_pkinase; 1. Probom; PD000001; Euk_pkinase; 1. PROSITE; PS00107; PROTEIN_KINASE_ATP; 1. PROSITE; PS00108; PROTEIN_KINASE_ST; 1. PROSITE; PS50011; PROTEIN_KINASE_DOM; 1. Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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11;

pkinase; 1.

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Pfam; PF00069;
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Matches 149;
                                                                                                                                            ACT_SITE
DOMAIN
SEQUENCE
                                                                                                                                                                                               Query Match
                                                                                                                   NP_BIND
BINDING
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                                                                             9
                                                                                                                     82 TLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVH 141
                                                                                                                                                                      200
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Subbaramaiah K., Greene V., Bartelt D.C.; "Structure of the cmkA gene encoding a CaMKII homolog in Emericella (Aspergillus) nidulans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kornstein L.B., Gaiso M.L., Hammell R.L., Bartelt D.C.;
Flooting and sequence determination of a cDNA encoding Aspergillus
nidulans calmodulin-dependent multifunctional protein kinase.";
Gene 113:75-82(1992).
                                                                                                                                                                                                                         223 DWWSVGIITYILLCGFEPFYDERGDQFWFRRILNCEYYFISPWWDEVSLNAKDLVRKLIV
                                                                                                       FMEV --- LGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRDSSLENEIAVLKKIKHENIV
                                                                                                                                                                                                           RDLKPENLLYLTPEENSKIMITDFGLSK-MEQNGIMSTACGTPGYVAPEVLAQKPYSKAV
                                                                                                                                                                                                                                                             DCWSIGVITYILLCGYPPFYEET-ESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLE
                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last anotation update)
Calcium/calmodulin-dependent protein kinase (EC 2.7.1.123) (CMPK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
--- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
--- SINILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CAMK SUBFAMILY:
                                                                             12;
                                                                                                                                                                                                                                                                                                                                        283 LDPKKRLTTFQALQHPWVTGKAANFVHMD---TAQKKLQEFNARRKLKAAVKA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella
  BY SIMILARITY.

CALMODULIN-BINDING (POTENTIAL).

EFEE51E5612326DC CRC64;
                                                    Length 473;
                                                                                                                                                                                                                                                                                                              260 KDPNERYTCEKALSHPWIDGNTA--LHRDIYPSVSLQIQKNFAKSKWRQAFNA
                                                                             87; Indels
                                                                 ; Pred. No. 6.1e-36; 53; Mismatches 87
                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                        414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Emericella nidulans (Aspergillus nidulans)
                                                    27.2%; Score 684;
48.1%; Pred. No. 6
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HSSP; 063450; 1A06.
Interpro; IPR000719; Euk_pkinase.
Interpro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                          51925 MW;
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                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
164
322
473 AA;
                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                            Matches 141;
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Q00771;
 ACT_SITE
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SEQUENCE
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                                                                  Local
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137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 RIEALKMO-----EEDEEDIPSAVDVQASEASDKSG----LSPFPALSTENSNTHPAST 362
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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MEDLINE=20541713; PubMed=11087665;
Brede G., Solhelm J., Troen G., Prydz H.;
"Characterization of PSKH1, a novel human protein serine kinase with centrosomal, golgi, and nuclear localization.";
Genomics 70:82-92(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77
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MEDILE-87092414; PubMed-2948189;
Hanks S.K.;
"Homology probing: identification of cDNA clones encoding members of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 RKTFIFMEVLGSGAFSEVFLVKQR--LTGKLFALKCIKKSPAFRDSSLENEIAVLKKIKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 KSLYRFGRTLGAGTYG---IVREADCSSGKVAVKIILKRNVRGNERMVYDELDLLQKLNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 ENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQN--GIMSTACGTPGYVAPEVLAQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 YSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316 HMRKLHMNLHSPGVRPEVENRPP--ETQASETSRPSSPEITITEAPVL--DHSVALPALT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                            Calmodulin-binding;
                                                                                                                                                                                                                                                                                                          SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                                                                                                                                                       Length 414;
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P11801; Q9NX19;
01-OCT-1989 (Rel. 12, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase H1 (EC 2.7.1.37) (PSK-H1).
                                                                                                                                                                                                                                                                                                       CALMODULIN-BINDING (BY SI
1E8D58A1C0B2F18C CRC64;
                                                                                                                                                                                                                       ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                         78; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
Prodm: PRODOUGH: EUK_pkinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE: PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS001108; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; Phosphorylation; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                    25.9%; Score 651; DB 1
38.3%; Pred. No. 6e-34;
                                                                                                                                                                                                 PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 QLPCQHGRRPTAPGG---RSLNCLVNGSL 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 ----GNGE----SGGTKKRSLSKIARGAI 383
                                                                                                                                                                                                                                                                                                                                   46889 MW;
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                                                                                                                                                                                                                                                                                                       291
414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Rasmussen C.D.;
                                                                                            CaMK-I)
                                                                                                                                                                                                    pombe.
                      RESULT 9
                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
ESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVHRDLKPE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLLYLTPEENSKIMITDFGLSKMEQNG---IMSTACGTPGYVAPEVLAQKPYSKAVDCWS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDPNE 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAAAVVHHMRKLHMNL 324
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                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (POTENTIAL)
PHOSPHORYLATION (AUTO-) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 424;
                                                                                                                                                                                                                                                            PERMIT PF00069; PKINASE; 1.
ProDom: PR000001; Buk_pkinase; 1.
ProDom: PR002001; Euk_pkinase; 1.
SWART: SW00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00110; PROTEIN_KINASE_ST; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine-fibreonine-protein kinase; ATP-binding; Phosphorylation; Golgi stack; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                        98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   B357757DDC12388D CRC64;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                      62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RMTALQALRHPWV------VSM----
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Interpro; IPR002290; Ser_thr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 -SQNLLKRASSRCQSTKSAQSTRSS 395
                                                                                                                                                                               EMBL; AJ272212; CAB91984.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                    48035 MW;
                                                                                                                                                                                          M14504; AAA36519.1;
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Matches 130; Conservative
                                                                                                                                                                                                          HSSP; Q63450; 1A06.
Genew; HGNC:9529; PSKH1.
MIM; 177015; -.
                                                                                                                                                                                                  PIR; B26368; B26368.
                                                                                                                                                                                                                                                                                                                                                                                                    424 AA;
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127
218
380
381
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MOD_RES
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BINDING
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MCCL_SCHEOLO

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can
                                                                                                                                                                                                                                                                                                                                             25.1%; Score 630; DB 1; Length 335;
43.6%; Pred. No. 9.7e-33;
tive 56; Mismatches 104; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             VLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPAFRDSSLENEIAVLKKI--KHENIVTLE 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase DCAMKL1 (EC 2.7.1.-) (Doublecortin-
Like and CAM Kinase-like 1).
DCAMKL1 OR KIAA0369.
                                                                                                                                    g; Phosphorylation.
291 PROTEIN KINASE.
293 ATP (BY SIMILARITY).
334 CALMODULIN-BINDING (POTENTIAL).
154 BY SIMILARITY.
192 PHOSPHORYLATION (AUTO-).
192 T->D: 15-FOLD INCREASE IN ACTIVITY.
115 E -> A (IN REF. 1).
295 KR -> NG (IN REF. 1).
38163 MW; 8761BBCFF6682B02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVHRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 KPENLLYLTPEENSKIMITDFGLSKMEQNG---IMSTACGTPGYVAPEVLAQKPYSKAVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 CWSIGVITYILLCGYPPFYEBTESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKc; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS0108; PROTEIN_KINASE_ST; 1.
ATP-binding; Serine/threonine-protein kinase; Transferase; Calmodulin-binding; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                740 AA.
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SEQUENCE FROM N.A. (ISOFORMS AS AND AL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       large proteins in vitro.";
4:141-150(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97349984; PubMed-9205841;
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                                                                                                                                                                         45
334
154
192
192
115
115
295
38163 MW;
                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 43.68 Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
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294
335 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DCK1_HUMAN
                                                                                                                                                                                                             ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                       CONFLICT
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LONG (AL) (SHOWN HERE), TYPE B SHORT (BS) AND LONG (BL): ARE PRODUCED BY ALTERNATIVE SPLICING. TYPE A AND TYPE B ISOPORMS DIFFER RESPECTIVELY BY THE PRESENCE OF ABSENCE OF THE DOUBLECORTIN DOMAIN. AN ALTERNATIVE SPLICING OCCURRING IN 3 OF THE MRNA PRODUCES THE LONG INSTEAD OF THE SHORT ISOFORMS.

1- TISSUE SPECIFICITY: IN FETAL TISSUES, HIGHLY EXPRESSED IN BRAIN, DETECTABLE IN LUNG AND LYPER, BUT NOT IN KIDNEY. IN ADDLT TISSUES, EXPRESSED UBIQUITOUSLY IN THE BRAIN DETECTABLE IN THE HEART. LIVER, SPLEEN, THYMES, PROSTATE, TESTIS, OVARY, SMALL INTESTINE AND COLON. THE TYPE A ISOFORMS SEEM TO BE EXPRESSED PREDOMINANTLY IN FETAL BRAIN WHEREAS TYPE B ISOFORMS ARE EXPRESSED ABUNDANTLY IN BOTH BRAIN.

1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Blainformatics and the BMBL outstation. the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY.
MEDLINE-99162404; Pubmed-10051403;
MATSUMOCO N., Pilz D.T., Ledbetter D.H.;
Matsumoto N., Pilz D.T., Ledbetter D.H.;
Genomic structure, chromosomal mapping, and expression pattern of human DCAMKL1 (KIAA0369), a homologue of DCX (XLIS).";
Genomics 56:179-183(1999).
-i- FUNCTION: PROBABLE KINASE THAT MAY BE INVOLVED IN A CALCIUM-
SIGNALING PATHWAY CONTROLING NEURONAL MIGRATION IN THE DEVELOPING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; TYPE A SHORT (AS) AND
                              MEDLINE-99156863; PubMed-10036192;
Sossey-Alaoui K., Srivastava A.K.;
"DCAMKLI, a brain-specific transmembrane protein on 13q12.3 that is
similar to doublecortin (DCX).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BRAIN. MAY ALSO PARTICIPATE IN FUNCTIONS OF THE MATURE NERVOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        !ransferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                    Omori Y., Suzuki M., Ozaki K., Harada Y., Nakamura Y., Takahashi E.-I., Fujiwara T.; Frada T.; Fujiwara T.; Fradassion and chromosomal localization of KIAA0369, a putative kinase structurally related to Doublecortin."; J. Hum. Genet. 43:169-177(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SER/PRO-RICH.
PROTEIN KINASE.
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS AS; AL; BS AND BL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS 2 DOUBLECORTIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neurogenesis; Alternative splicing.

DOMAIN 57 143 DOUBLECORTIN 1.

DOMAIN 186 269 DOUBLECORTIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probon; PD000001; Euk_pkinase; 1.
SMART; SM0537; DCX; 2.
SMART; SM0220; S_TKC; 1.
SMO120; S_TC; 1.
PROSITE; PS50309; DC; 2.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM: 604742; -.
InterPro; IPR003533; DCX.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfan; PF00069; pkinase; 1.
Pfan; PF03607; DCX; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00108; PROTEIN_KINASE_ST;
                                                                                                                                                                                                                                                                                                                                          MEDLINE=98419166; PubMed=9747029;
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                                                                                                                                                                                                       Genomics 56:121-126(1999)
TISSUE-Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; Q63450; 1A06
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DOMAIN
NP_BIND
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us-09-960-643-2.rsp

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PROSITE; PS00108;
                                                                                                                                                                                                                                           Neurogenesis
                                                                                                                                                                                                                                                                                                                    ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
DOMAIN
NP_BIND
                                                                                                                                                                                                                                                                                                                                                      Query Match
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KCCB_HUMAN
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                                                                         SSSETVRSPNSPF -> LDHGFTIKRSGSLDYYQQPGMYWI
                                                                TTALDKERQVFRRRRNQDVRSRYKAQPAPPELNSESEDYSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPING
                                                                                                                                                                                     264
                                                                                                                                                                                                                                                                                                                      694
                                                                                                                                                                                                                   ESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVHRDLKPE 147
                                                                                                                                                    Gaps
                                                                                                                                                                        LGSGAFSEVFLVKQRLTGKLFALKCIKKSPA-FRDSSLENEIAVLKKIKHENIVTLEDIY 87
                     POLY-ARG.
MISSING (IN ISOFORM BS AND ISOFORM BL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase DCAMKL1 (EC 2.7.1.-) (Doublecortin-DCAMKL1 OR DCLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Neurosci. Res. 58:567-575(1999).

-!- FUNCTION: PROBABLE KINASE THAT MAY BE INVOLVED IN A CALCIUM-
SIGNALING PATHWAY COWTROLLING NEGRONAL MIGRATION IN THE DEVELOPE
BRAIN: MAY ALSO PARTICIPATE IN FUNCTIONS OF THE MATURE NERVOUS
SYSTEM (By similarity).

-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                 : : ||||:|| |||||:||| 456 DVPTELYLVMELVKGGDLFDAITSTNKYTERDASGMLYNLASAIKYLHSLNIVHRDIKPE
                                                                                                                                                                                                                                                             NILYLTPEENSK-IMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQKPYSKAVDCWSIG
                                                                                                                                                                                                                                                                          VITYILLCGYPPF -- YEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDPNE
                                                                                                                                                                                                                                                                                                                                                   265 RYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNF------AKSKWR
                                                                                                                                                                                                                                                                                                                                                                        635 RFSAVQVLEHPWVNDDGLPENEHQLSVAGKIKKHFNTGPKPNSTAAGVSVIATTALDKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                           PASTSS -> MLELIE (IN ISOFORM BS AND ISOFORM BL).
                                                                                                                             Score 612; DB 1; Length 740;
Pred. No. 3.4e-31;
69; Mismatches 107; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burgess H.A., Martinez S., Reiner O.; "KIAA0369, doublecortin-like kinase, is expressed during brain
                                                                                                                                                                                                                                                                                                                                                                                             306 QAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPETQA-SETSRPSSPE 352
                                                                                                                                                                                                                                                                                                                                                                                                          ISOFORM BS).
D7B6D855099A315C CRC64;
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        756 AA
            SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
MEDLINE=20004649; PubMed=10533048;
                                                                                                         82223 MW;
                                                                                                                              24.48;
                                                                                                                                                   136; Conservative
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419
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701
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313
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                                                                                                         740 AA;
                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAMK SUBFAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
419
511
698
                                 1
308
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BINDING
ACT_SITE
DOMAIN
                                                                                                         SEQUENCE
                               VARSPLIC
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                                                              VARSPLIC
                                                                                                                              Query Match
                                                                                                                                          Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   686 NIGPKPSSTAAGVSVIATTALDKERQVFR------RRRNQDVRS---RYKAQPAPPEL 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 WKKQTT-----NIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPA-FRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |::: : | : : | | : : | | : : | | : | 387 WRREESEEGFQIPATITERYKVGRTIGDGNFAVVKECIERSTAREYALKIIKKSKCRGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 VIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSK-IMITDFGLSKMEQNGIMSTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 SPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -------AKSKWRQAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPET

        ACCB_HUMAN
        STANDARD;
        PRT;
        664 AA.

        Q13554;
        O95437;
        O95599;
        Q9UGH7;
        Q9UGH9;
        Q9UNXO;

        Q9UNX7;
        Q9PG00;
        Q9Y5N4;
        Q9Y6F4;
        Created)
        O1-NOV-1997 (Rel. 35, Created)
        Created)
        A16-CCT-2001 (Rel. 40, Last sequence update)

        15-JUN-2002 (Rel. 41, Last annotation update)
        A11, Last annotation update)
        A12, Last annotation update)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.1%; Score 606; DB 1; Length 75
36.7%; Pred. No. 8.2e-31;
ive 76; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
3D1DBF18C23129F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOUBLECORTIN 1. DOUBLECORTIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOUBLECORTIN
SER/PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN_KINASE_ATP; 1.
PROTEIN_KINASE_DOM; 1.
PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                               Interpro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
Pfam; PF03607; DCX; 2.
                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                             InterPro; IPR003533; DCX.
InterPro; IPR000719; Euk_pkinase
                                                                                                                                                                   EMBL; AF155819; AAF26673.1; -. HSSP; Q63450; 1A06.
MGD; MGI:1330861; Dcamkll.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84153 MW;
                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00537; DCX; Z.
SMART; SM00220; S_TKc; 1.
PROSITE; PS50309; DC; Z.
PROSITE; PS00107; PROTEIN_K1
PROSITE; PS5011; PROTEIN_K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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269
358
663
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298
406
412
435
527
756 AA;
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Matches 137; Conserv
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us-09-960-643-2.rsp

AJ252236; CAB65120.1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [5]
SEQUENCE OF 302-603 FROM N.A. (ISOFORM 1).
MEDLINE-97214619; PubMed-9060999;
Tombes R.M., Krystal G.W.;
Tombes R.M., Krystal G.W.;
"Identification of novel human tumor cell-specific CamK-II variants.";
Biochim. Biophys. Acta 1355:281-292(1997).
-i- FUNCTION: THIS KINASE MAY PLAY A ROLE IN NEUROTRANSMISSION.
-i- CATALYTIC ACTYLY: ATP + protein = ADP + 0-phosphoprotein.
-i- ENZYME REGULATION: AUTOPHOSPHORYLATION OF CAM-KINASE II PLAYS AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
-i- SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE PRODUCTS: 7 ISOFORMS; 0/BETA, 1/BETA1/BETA'E, 2/BETA2, 3 (SHOWN HERE), 4/BETA4/BETAE, 6/BETA6 AND 7/BETA7; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                             the beta subunit
II with different
2.7.1.123) (CaM-kinase II beta chain (EC (CaMK.II) (CaM-kinase II beta subunit) (CaMK.II beta subunit). CAMK2B OR CAMKB OR CAMKB OR CAMMA. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20277365; PubMed=10819240; Rochlitz H., Voigt A., Lankat-Buttgereit B., Goke B., Heimberg H., Nauck M.A., Schlemann U., Schatz H., Pfeiffer A.F.; "Cloning and quantitative determination of the human Ca2+/calmodulin-dependent protein kinase II (CaMK II) isoforms in
                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CAMK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                            Li G.Y., Cooper N.G.F.; "Moccular cloning and sequencing of human calcium/calmodulin adopendent protein Kinas II beta subunit."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                   TISSUE-Skeletal muscle;
Leddy J.J., Salih M., Tuana B.S.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                          Wang P., Wu Y., Zhou T.H., Sun Y., Pei G.; "Identification of alternative splicing variants of of human Ca(2+)/calmodulin-dependent protein kinase
                                                                                                                                                 [1]
SEQUENCE FROM N.A. (ISOFORMS 0; 1; 4; 6 AND 7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 0 AND 4).
                                                                                                                                                                                             MEDLINE-20317016; PubMed-10858498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF081572, AAD42036.1; --
EMBL, AF083419; AAD42038.1; --
EMBL, AF081924; AAD42037.1; --
EMBL, AF140350; AAD42070.1; --
EMBL, AF112472; AAD93744.1; --
EMBL, AF112472; AAD93744.1; --
EMBL, AF112471; AAD03743.1; --
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diabetologia 43:465-473(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF078803; AAD42035.1; -.
                                                                                                                                                                                                                                                                       FEBS Lett. 475:107-110(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Insulinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human beta cells."
                                                                                                                               NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                               rissue-Brain;
                                                                                                                                                                                rissue-Brain
                                                                                                                                                                                                                                                            activities."
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12;
                                                                                                                                                                                                                                                                                                                                                                       ISSING (IN ISOFORM 1, ISOFORM 2 AND ISSING (IN ISOFORM 7).
MISSING (IN ISOFORM 7).
MISSING (IN ISOFORM 6).
MISSING (IN ISOFORM 1).
MISSING (IN ISOFORM 1).
MISSING (IN ISOFORM 0, ISOFORM 2, ISOFORM 4, ISOFORM 6, ISOFORM 6).

L -> V (IN REF. 3).
K -> N (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| :| :| :| :| :| 367 TMLATRNFSVGRQTTAPATMSTAASGTTMGLVEQAKSL-LNKKADGVKPQTNSTKNSAAA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNF-AKSKWRQAF-- 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340 TQASETSRPSS--PEITITEAPV------LDHSVALP----ALTQLPCQHGR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 IKHENIVTLEDIYESTTHYYLVMQLVSGELFDRILERGVYTEKDASLVIQQVLSAVKYL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 THIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI--KKSPAFRDSSLENEIAVLKK 74
                                                                                                                                                                                                                         FROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

CAMADOLIN-BINDING.

V -> A (IN ISOFORM 1, ISOFORM 2 AND ISOFORM 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 NLINOMLTINPAKRITAHEALKHPWVCQRSTVASMMHRQETVECLKKFNARRKLKGAILT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 HENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMST---ACGTPGYVAPEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 AQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAK
                                                                                                                                                                                                        Transferase; Serine/threonine-protein kinase; Calmodulin-binding; Phosphorylation; ATP-binding; Neurone; Alternative splicing.

DOMAIN 272 PROTEIN KINASE.

NP_BIND 20 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  380 R----PTAPGGRSLNCLVNGSLHISSSL-----VPMHQGSLAAGPCGCCSSCL 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSRGAPACPSPAPFSPLPAPSPRISDILNSVRRGSGTPEAEGPLSAGPPPCLSPAL 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.0%; Score 603.5; DB 1; Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9E8C82918D986814 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1e-30;
                                                                                                                                 ProDom; PD000001; EUK_pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
EMBL; AJ252237; CAB65121.1; -.
EMBL; AJ25233; CAB65122.1; -.
EMBL; AJ25233; CAB65122.1; -.
EMBL; U50358; AAB16663.1; -.
Genew; HGNC:1461; CAMK2B.
INTECPFO; IPR000719; EUk_pkinase.
InterPro; IPR002290; ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72726 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              582
68
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301
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393
531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68
533
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379
410
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BINDING
ACT_SITE
DOMAIN
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VARSPLIC
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RESULT 13 DCK1_RAT

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                                                  | ||:||::|:|||: | :| :|: ::|:: : ||||:: : : ||:: :|:|
FPSPYWDNVSDSAKELINMMLLVNVDQRFSAVQVLEHPWVNDDGLPENEHQLSVAGKIKK 360
                                                                                                                                                                                                                    -----AKSKWRQAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPP 338
                      CGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPF--YEETESKLFEKIKEGYYE 237
                                                                                                                                                                                                                                                                 361 HFNTGPKPSSTAAGVSVIATTALDKERQVFR-----RRRNQDVRG---RYKAQPAPP 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0900M7: 091352;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 44). Last annotation update)
Calcium/calmodulin-dependent protein kinase type II alpha chain (EC
2.7.1.123) (CaM-kinase II alpha chain) (CaM kinase II alpha subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Human calcium/calmodulin-dependent protein kinase II: cDNA cloning
                                                                                                                      238 FESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: THIS KINASE MAY PLAY A ROLE IN NEUROTRANSMISSION.
-i- CARALYTIC ACTIVITY: ATP + protein = ADP + 0-phosphoprotein.
-i- ENYME REGULATION: Autophosphorylation of Thr-286 allows the kinase to switch from a calmodulin-dependent to a calmodulin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are produced by alternative splicing.
-i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and gene analysis.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              independent state (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00108; PROTEIN_KINASE_ST; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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InterPro; IPR002290; Ser_thr_pkin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF145710; AAD30558.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF145711; AAD30559.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:1460; CAMK2A.
MIM; 114078; -.
                                                                                                                                                                                                                                                                                                                    ETQA-SETSRPSSPE 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CaMK-II alpha subunit).
                                                                                                                                                                                                                                                                                                                                                                 ELNSESEDYSPSSSE 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
Li G.Y., Cooper N.G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAMK SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND DELTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            063450;
                                                                                                                                                                                                                    NF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KCCA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAMK2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP;
                                                                                                                                                                                                                                                                                                                 339
                                                                                                                                                                                                                                                                                                                                                                 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KCCA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                    301
                         180
                                                                                                                                                                                                                    298
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                               Hevroni D., Rattner A., Bundman M., Lederfein D., Gabarah A., Mangelus M., Silverman M.A., Kedar H., Naor C., Kornuc M., Hanoch T., Seger K., Theill L.E., Nedivi E., Richter-Levin G., Citri Y.; Hippocampal plasticity involves extensive gene induction and multiple cellular mechanisms.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: PROBABLE KINASE THAT MAY BE INVOLVED IN A CALCIUM-SIGNALING PATHWAY CONTROLING NEURONAL MIGRATION IN THE DEVELOPING BRAIN. MAY ALSO PARTICIPATE IN FUNCTIONS OF THE MATURE NERVOUS SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSK-IMITDFGLSKMEQNGIMSTA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ||: :: || ||| || || GPGEESDEGFQIPAT-ITERYKVGRTIGDGNFAVVKECIERSTAREYALKIIKKSKCRG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEHMIQNEVSILRRVKHPNIVLLIEEMDVPTELYLVMELVKGGDLFDAITSTSKYTERDA 181
                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPA-F 60
                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Serine/threonine-protein kinase DCAMKLI (EC 2.7.1..) (Doublecortin-like and CAM kinase-like 1) (Calcium/calmodulin-dependent protein kinase type I-like CPG16).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.0%; Score 602.5; DB 1; Length 433; 37.1%; Pred. No. 7e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000719; Buk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Prom; PP00069; pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SER/PRO-RICH (BY SIMILARITY)
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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433 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Wistar;
MEDLINE=98364306; PubMed=9699150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Neurosci. 10:75-98(1998)
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                                                                                                                                                                                                                    Rattus norvegicus (Rat).
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340
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433 AA;
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Matches 139; Conser
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurogenesis
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SEQUENCE
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NP_BIND
BINDING
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                                                                                                                                                                                                                                                                              DFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNF-AKSKWRQAFNA 310
                                                                                                                                                                                                                                                                                                                    HENGIVHROLKPENLLYLTPEENSKIMITDFGLS---KMEQNGIMSTACGTPGYVAPEVL 191
                                                                                                                                                                                                                                                                                                                                    ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                         192 AQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAK 251
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                              75 IKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                  7 TRFTEEYQLFEELGKGAFSVVRRCVKVLAGQEYAAKIINTKKLSARDHQKLEREARICRL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1989 (Rel. 11, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Calcium/calmodulin-dependent protein kinase type II alpha chain (EC 2.7.1.123) (CaM-kinase II alpha chain) (CaM kinase II alpha subunit).
                                                                                                                                                                                                          17 TNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI--KKSPAFRDSSLENEIAVLKK 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-87289722; PubMed-3475713;
Lin C.R., Kapiloff M.S., Durgerian S., Tatemoto K., Russo A.F.,
Lanson P., Schulman H., Rosenfeld M.G.;
"Molecular cloning of a brain-specific calcium/calmodulin-dependent
protein kinase.";
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MEDLINE-87263392; PubMed-3037704;
Hanley R.M., Means A.R., Ono T., Kemp B.E., Burgin K.E., Waxham N.,
                                                                                                                                                                                                                                                                                                                                                                                           Kelly P.T.; "Punctional analysis of a complementary DNA for the 50-kilodalton subunit of calmodulin kinase II.";
Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
                                                                                                                                                                               10;
                                                                                                           -> KKRKSSSSVQLM (IN ISOFORM B).
10800A85CAD724BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355
                                                                                                                                                    Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357
                                                                                                                                                  24.0%; Score 602; DB 1; Length 470
39.1%; Pred. No. 8.4e-31;
.ive 58; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 AAVVHHM---RKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 IMLATRNFSGGKSGGNKKSDGVKESSESTNTTIEDEDTKVRKQEIIKVTE
        Alternative splicing. PROTEIN KINASE.
                                                                                              CALMODULIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 84:5962-5966(1987)
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                  277
19 27
12 42
5 135
286
328
328
54029 MW;
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           hosphorylation; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 237:293-297(1987).
                                                                                                                                                                 Best Local Similarity 39.19
Matches 137; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                 135
286
290
328
478 AA;
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                                     NP_BIND
BINDING
ACT_SITE
MOD_RES
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SEQUENCE
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                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKHPNIVRLHDSISEEGHHYLIFDLVTGGELFEDIVAREYYSEADASHCIQQILEAVLHC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HENGIVHRDLKPENLLYLTPEENSKIMITDFGLS----KMEQNGIMSTACGTPGYVAPEVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: |:||||||||||| : :::||||| HQMGVVHRDLKPENLLLASKLKGAAVKLADFGLAIEVEGEQQAWFGFA-GTPGYLSPEVL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                    independent state.
-1- SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA,
               Sunyer T., Sahyoun N.; "Sequence analysis and DNA-protein interactions within the 5' flanking region of the Ca2+/calmodulin-dependent protein kinase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CAMK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CALMODULIN-BINDING.
G -> A (IN REF. 2).
306F416CCE9B5F62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (AUTO-).
                                                                                                       SEQUENCE OF 282-299, AND PHOSPHORYLATION OF THR-286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J02942; AAA41870.1; -.
EMBL; M16660; AAA41855.1; -.
EMBL; M30959; AAA40841.1; -.
PIR; A31215; A31235.
PIR; A30355; A30355.
HSSP; Q63450; IA06.
InterPro; IPR0007019; Euk_pkinase.
InterPro; IPR000290; Ser_thr_pkinase.
InterPro; IPR00290; Ser_thr_pkinase.
ProDom; PF00069; pkinase; 1.
ProDom; PF00069; Euk_pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/Threoning-Protein kinase; Call Phosphorylation; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.8%; Score 599; DB 1; 38.9%; Pred. No. 1.3e-30;
                                                                         Proc. Natl. Acad. Sci. U.S.A. 87:278-282(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN KINASE
MEDLINE=90115857; PubMed=2153289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54114 MW;
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290 3
301 3
                                                            alpha-subunit gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                    AND DELTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 136;
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BINDING
ACT_SITE
MOD_RES
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Best Local
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 Dp
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Qy
Dp
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311 AAVVHHM---RKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITE 357 : | | : | | : | | : | | 306 TMLATRNFSGGKSGGNKKNDGVKESSESTNTTIEDEDTKVRKQEIIKVTE 355 oy Oy

Search completed: March 14, 2003, 14:08:58 Job time: 17 secs

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			i

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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using sw model - protein search, OM protein

March 14, 2003, 14:07:31; Search time 18 Seconds (without alignments) 2542.221 Million cell updates/sec Run on:

Title:

.....VKASGSSHCRAGQTGVCLIM 476 US-09-960-643-2 2513 1 MGRKEEDDCSSWKKQTTNIR... Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

PIR_73:* Database :

pir1:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ca2+/calmodulin-de prottein KNO9.2 [1 calmodulin-binding ca2-/calmodulin-de ca2+/calmodulin-de ca2+/calmodulin-de myosin-light-chain ca2+/calmodulin-de myosin-light-chain ca2+/calmodulin-de hypothetical prote Ca2+/calmodulin-de Ca2+/calmodulin-de Ca2+/calmodulin-de Ca2+/calmodulin-de Ca2+/calmodulin-de Ca2+/calmodulin-de Description SUMMARIES S57347 11321321 1156542 1156542 1130814 1152637 115263 T23614 S43845 B46619 A45025 A26464 S50193 Length DB 44421 4469 4473 4414 4414 4414 447 650 650 650 6533 447 Query Match I 1155.5 1152.5 1004 Score 980 736 736 692.5 691.5 691.5 691.5 691.5 692.9 693.0 694.5 693.0 694.5 693.0 694.5 693.0 694.5 693.0 694.5 693.0 694.5 693.0 694.5 Result Ş.

Ca2+/calmodulin-de	calcium-dependent	probable serine-th	Ca2+/calmodulin-de	calcium-dependent	protein kinase RAD	calcium-dependent	calcium-dependent	probable calcium d	probable calcium-d	hypothetical prote	protein-serine kin	calcium-dependent	calcium-dependent	calcium-dependent	calcium-stimulated
A40896	T05476	T38226	A31908	S71776	A39616	A49082	T08873	F85059	H84810	T33690	138138	A43713	S46284	T02139	S54788
7	7	7	Н	, ,	~	, ,	~	7	7	7	7	H	1	7	7
446	554	504	527	490	821	610	490	520	583	443	319	208	495	553	591
23.0	22.8	22.7	22.5	22.3	22.2	22.1	22.0	21.7	21.7	21.6	21.6	21.6	21.6	21.5	21.5
'n.	573	569.5	566.5	559.5	558	556.5	553	546.5	544.5	544	543.5	543.5	543	541.5	541.5
577															

ALIGNMENTS

RESULT 1

S50193
Ca2+/Calmodulin-dependent protein kinase (EC 2.7.1.123) I - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: S50193; A49682; A46038
R;Cho, F.S.; Phillips, K.S.; Bogucki, B.; Weaver, T.E.
Biochim. Biophys. Acta 1224, 156-160, 1994
Afitie: Characterization of a rat CDNA Clone encoding calcium/calmodulin-dependent
A) Keteretice indiper: SJOLY3; MOLD:930433113; FMID:/948036
A: Status: preliminary
A; Molecule type: mRNA
A;Residues: 1-374 <cho></cho>
A;Cross-references: EMBL:L26288; NID:g439613; PIDN:AAA66944.1; PID:g439614
R; Picciotto, M.R.; Czernik, A.J.; Nairn, A.C.
J. Biol. Chem. 268, 26512-26521, 1993
A;Title: Calcium/Calmodulin-dependent Protein kinase i. cDNA cloning and identificat
A: ACCESSION: A49682 MOID: 940/3341; FMID: 0235/00
A.Status. proliminary
A: Wolecule type: mRNA
A; Residues: 1-111, G', 113-117, 'R', 119-308, 'R', 310-322, 'HOPG', 327, 'T', 329, 'TDS' <pic:< td=""></pic:<>
A; Cross-references: GB:L24907; NID:q406112; PIDN:AAA19670.1; PID:q406113
R; Mochizuki, H.; Ito, T.; Hidaka, H.
J. Biol. Chem. 268, 9143-9147, 1993
A;Title: Purification and characterization of Ca2+/calmodulin-dependent protein kina
A; Reference number: A46038; M0ID:93232082; PMID:8386178
A, Accession: A46038
A;Status: preliminary
A; Molecule type: protein
A; Residues: 12-36, 'T' <moc></moc>
A) Experimental source: cerebrum
A;Note: sequence extracted from NCBI backbone (NCBIP:12992/)
C; Superramily: Cal-/calmodulin-dependent protein kinase 1; protein kinase nomology
C.Negwords: Arr; dutcpinospinoffaction; calmoduiin binding; phosphotein; phosphotic Tring-276/Domain: profesh kinase homology (KIN)
F:26-34/Region: protein kinase ATP-binding motif
F;293-299/Region: autoinhibitory
F;302-314/Region: calmodulin binding
F:177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred
Query Match 46.0%; Score 1155.5; DB 1; Length 374;
į
Matches 222; Conservative 43; Mismatches 51; Indels 3; Gaps 3;
QY 12 WKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPAFRDSSLENEIA 70
DD 10 W-KQAEDIRDIYDFRDYLGTGAFSEVILAEDRRTQKLVAIKCIAKKALEGKEGSMENEIA 68

71 VLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSA 130

С ŏ

Db 69 VLHXIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQVLDA 128	
131 VKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMSTACGTPGYVAPE 189 :	OY 370 LTQLPCQHGRRPTAPGGRSLNCLVNGSLHISSSLVPMHQGSLAAGPCGCCSSCLNIGSKG 429 DD 325QEGQGQTASHGELLTPVAGGPAAG-C-CCRDC 354
190 VLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISES 249 	Oy 430 KSSYCSEP 437 1 1 Db 355CVEP 358
250 AKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFN 309 	RESULT 3 T37321 G374 Calmodulin-domandont protein Pinsce (EC 2.7.1.123) I - Caenorhabditis elegans
310 AAAVVHHMRKLHMNLHSPG 328 	.unoutill dependent plotein Ainase (bc 2.7.1.122) 1 22 Caenorhabditis elegans 03-bec-1999 #sequence_revision 03-bec-1999 #text_cha sion: T37321 N.: Kimura, Y.: Masuho, Y.: Arai, K.:
RESULT 2 S\$7347 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - human N.Alternate names: CaMKI C.Species: Homo sapiens (man)	J. Biol. Chem. 274, 22556-22562, 1999 A; Title: Ca2+/calmodulin-dependent protein kinase cascade in Caenorhabditis elegans. A; Reference number: Z21686; MUID:99357789; PMID:10428833 A; Accession: T37321 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C; Accession: \$57347 R; Haribabu, B.; Hook, S.S.; Selbert, M.A.; Goldstein, E.G.; Tomhave, E.D.; Edelman, A.M. EMBO J: 14, 3679-3886, 1995 A; Title: Human calcium-calmodulin dependent protein kinase I: cDNA cloning, domain struct	A; Residues: 1-348 <eto> A; Residues: 1-348 <eto> A; Cross-references: EMBL.AB021864; NID:95672677; PIDN:BAA82674.1; PID:95672678 A; Experimental source: strain Bristol N2; embryonic stage C; Genetics: A; Note: cmk-1</eto></eto>
sference number: S57347; MUID:95369239; PMID:7641687 ccession: S57347	C;Superfamily: Ca2+/calmodulin-dependent protein Kinase I; protein Kinase homology C;Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotran
Status: preliminary; nucleic acid sequence not shown Molecule type: mRNA Residues: 1-370 <hara< td=""><td>Query Match 40.0%; Score 1004; DB 2; Length 348; Best Local Similarity 57.3%; Pred. No. 2.5e-37; Matches 185; Conservative 67; Mismatches 69; Indels 2; Gaps 2;</td></hara<>	Query Match 40.0%; Score 1004; DB 2; Length 348; Best Local Similarity 57.3%; Pred. No. 2.5e-37; Matches 185; Conservative 67; Mismatches 69; Indels 2; Gaps 2;
, ,	QY 19 IRKTFIFMEVLGSGAFSEVFLVKQRL-TGKLFALKCI-KKSPAFRDSSLENEIAVLKKIK 76
Superiminity: Carl/Cainmodulin-dependent protein kinase 1; protein kinase nomology Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransfe 18-276/Domain: protein kinase homology cKIN» 26-34/Region: protein kinase ATP-binding motif	QY 77 HENIVTLEDIYESTTHYYLVWQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHE 136
293-299/Region: autoinhibitory 302-314/Region: calmodulin binding 177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicte	Qy 137 NGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQKPY 196
Ouery Match 45.9%; Score 1152.5; DB 1; Length 370; Best Local Similarity 55.8%; Pred. No. 9.2e-44; Matches 239; Conservative 46; Mismatches 62; Indels 81; Gaps 9;	
12 WKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLJGKLFALKCI-KKSPAFRDSSLENEIA 70 	257 LLEKDPNERYTCEKALSHPWIDGNTALHRDIVPSVSLQIQKNFAKSKURQAFNAAAVVHH
71 VLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSA 130 	317 MRKLHMNLHSPGVRPEVENRPPE 339 3.1 ALL ST. S.
131 VKYLHENGIVHRDLKPENLIZLIPEENSKIMITDFGLSKMEQNG-INSTACGTPGYVAPE 189 	SULT 4
190 VLAQRPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYVEFESPFWDDISES 249 	Deceden K07A9.2 [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-Aug-2001
	R; anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998 A;Title: Genome sequence of the nematode C. elegans: a platform for investigating blo A;Reference number: AST5000; MUID:99069613; PMID:9851916 A;Note: sea waheites genome unstl edu/ges/C. elegans/and www.sanderac.ink/Projects/C.
310 AAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPETTITEAPVLDHSVALPA 369	A;Note: see Websites genome.Wusti.edu/gsc/C_elegans/ and Www_sanget.ac.ux/riojecus/C_

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C; Species: Fugu rubripes
C; Species: Fugu rubripes
C; Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 03-Jun-2002
C; Accession: T30814
R; Cottage, A.J.; Clark, M.; Hawker, K.; Umrania, Y.; Wheller, D.; Bishop, M.; Elgar, FEBS Lett. 443, 370-374, 1999
A; Title: Three receptor genes for plasminogen related growth factors in the genome of A; Reference number: Z20880; MuID: 99148833; PMID: 10025966
A; Accession: T30814
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-421 <COT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL:AJ010348; NID:e1355080; PID:e1355083; PIDN:CAA09101.1 C; Genetics: A; Introns: 32/2; 76/2; 101/2; 147/3; 186/1; 211/2; 257/1; 283/2; 312/3
                                                                                 311 AKWKKAVRVTTLMKRLR-----GAA 346
                                                                                                                                                                                                                                     ---RSLNCLVNGSL--HISSSLV 404
                                                                                                                                                                                                                                                                               347 GGAVAAAAGGAAPASGASATVGTGGDAGCAAKSDDMASADRSATPATDGSATPATDGSVT 406
                                                                                                                                                                                                                                                                                                                           PMHQGSLAAGPCGCCSSCLN----IGSKGKSSYCSEPTLLKKANKKQNFKSEVMV---PV 457
                                                                                                                                                                                                                                                                                                                                                                PATDGSITPATDGSVTPATDRSATPATDGRATPATEESTVPAAQSSAAPAAKAAATPEPA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 IYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVHRDLK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 PENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQKPYSKAVDCWSI 205
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                                                        FWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAK 301
                                                                                                                                              SKWRQAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAPVL 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVITYILLCGYPPFY----EETESK---LFEKIKEGYYEFESPFWDDISESAKDFICHL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAAAVVHHM 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 EVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFR-DSSLENEIAVLKKIKHENIVTLED 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.0%; Score 703; DB 2; Length 42 38.4%; Pred. No. 3.8e-24; Live 83; Mismatches 138; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            calmodulin-binding protein kinase - Fugu rubripes
                                                                                                                                                                                                                                  362 DHSVALPALTQLPCQHGRRPTAPGG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 28.0°
Best Local Similarity 38.4°
Matches 154; Conservative
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156542
calmodulin-binding protein - rat
calmodulin-binding protein - rat
C; Species: Rattus norvegicus (Norway rat)
C; Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Sep-1999
C; Accession: 156542
R; Godbout, M.; Erlander, M.G.; Hasel, K.W.; Danielson, P.E.; Wong, K.K.; Battenberg, E.I.
J; Neurosci. 14, 1-13, 1994
A; Title: 165: a calmodulin-binding, vesicle-associated, protein kinase-like protein enri
A; Reference number: 156542; MUID:94110847; PMID:828328
A; Accession: 156542
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-504 <RES>
A; Cross-references: GB:L22557; NID:9349074; PIDN:AAA16633.1; PID:9349075
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc
C; Reywords: calmodulin binding
F; 22-286/Domain: protein kinase homology <KIN>
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A.Accession: B88640
A.Accession: B88640
A.Status: preliminary
A.Status: preliminary
A.Wolecule type: DNA
A.Residues: 1-310 <STO>
A.Koross: references: GB:chr_IV; PIDN:AAC68810.1; PID:g3790765; GSPDB:GN00022; CESP:K07A9.C; Genetics:
A.Gene: K07A9.2
A.Wap position: 4
C; Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 AVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 AVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPE 189
                                                                                                                                                                                                                                                                                                                                              NEIAVLK----KIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASL 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLAQKPYSKAVDCWSIGVITYILLCGYPPYEBTE-----SKLFEKIKEGYYEFESP
|: :: | : ||||:|||| |||| | |||||| |
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                                                                                                                                                                                                                                                       Length 310;
                                                                                                                                                                                                                                                   ; Score 880; DB 2; Length 31; Pred. No. 5.6e-32; 55; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KWRQAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPE 339
                                                                                                                                                                                                                                                     Query Match 35.0%;
Best Local Similarity 57.4%;
Matches 159; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                    123
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N; Alternate names: Ca2+/calmodulin-dependent protein kinase Gr
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A; Residues: 1-37 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         und in sperm cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: 149571
A; Accession: 149571
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 250-277, CEC1', 281-301, 'T', 303-338, 'X', 340-469 <RES>
A; Cross-references: GB:J03057; NID:g192365; PIDN:AAA37366.1; PID:g192367
A; Cross-references: GB:J03057; NID:g192365; PIDN:AAA37366.1; PID:g192367
A; Cross-references: GB:J03057; NID:g192365; PIDN:AAA37366.1; PID:g192367
C; Keywords: alternative splicing; ATP; calmodulin binding; phosphotransferase; serine/thf R; A0-296/Domain: protein kinase homology < KIN>
F; 40-296/Domain: protein kinase APP-binding motif F; 306-468/Product: calspermin #status predicted <CSP>
F; 318-337/Region: calmodulin binding #status predicted
F; 71/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                     A Accession: $17656

A; Molecule type: mRNA
A; Residues: 1-469 <-Jone
A; Esterances: EMBL:X88995; NID:950366; PIDN:CAA41741.1; PID:950367
B; Sikela, J.M.; Hahn, W.E.
B; Sikela, J.M.; Hahn, W.E.
A; Title: Screening an expression library with a ligand probe: isolation and sequence of A; Reference number: A29878; MUID:87204263; PMID:3033675
A; Recession: A29878
A; Accession: A29878
A; Molecule type: mRNA
A; Residues: 315-469 <-SIK>
A; Cross-references: GB:M16206; NID:9200360; PIDN:AAA39933.1; PID:9387512
A; Cross-references: GB:M16206; NID:9200360; PIDN:AAA39933.1; PID:9387512
A; Sikela, J.M.; Law, M.L.; Kao, F.
Genomics 4, 21-27, 1989
A; Title: Chromosomal localization of the human gene for brain Ca2+/calmodulin-dependent
A; Reference number: 149571; MUID:89122027; PMID:2536634
                                                                                                                                                                                                                                                                                             A;Title: cDNA sequence and differential expression of the mouse Ca(2+)/calmodulin-dependa; Reference number: S17656; MUID:91372388; PMID:1893997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                             C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S1765, A29878; I49571
K;Jones, D.A.; Glod, J.; Wilson-Shaw, D.; Hahn, W.E.; Sikela, J.M.
FEBS Lett. 289, 105-109, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 NCEYYFISPWWDEVSLNAKDLVKKLIVLDPKKRLTTFQALQHPWVTGKAANFVHMD---T 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKSPAFRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 YTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSK-MEQN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 GIMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEET-ESKLFEKIK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 VLMKTVCGTPGYCAPEILRGCAYGPEVDMWSVGIITYILLCGFEPFYDERGDQFMFRRIL 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTA--LHRDIYPS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 CSSWKKQTTNIRKTF-----IFMEV---LGSGAFSEVFLVKQRLTGKLFALKCI 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 469;
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                                                                                              protein kinase (EC 2.7.1.123) IV
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42.7%; Pred. No. 7.2e-24;
11ve 60; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                              Ca2+/calmodulin-dependent
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Best Local Similarity
Matches 152; Conserv
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N; Contains: calspermin (Norway rat) All Contains: calspermin (Software) (Sof
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A; Residues: 250-474 C0H3>
A; Residues: 250-474 C0H3>
A; Cross-references: GB:J04600; NID:g206172; PIDN:AAA41867.1; PID:g206173
A; Cross-references: GB:J04600; NID:g206172; PIDN:AAA41867.1; PID:g206173
B; Means, A.R.; Cruzalegui, F.; LeMagueresse, B.; Needleman, D.S.; Slaughter, G.R.; On Mol. Cell. Biol. 11, 3960-3971, 1991
A; Title: A novel Ca(2+)/Calmodulin-dependent protein kinase and a male germ cell-spec A; Recession: A41250; MUID:91304387; PMID:1649385
A; Molecule type: mRNA
A; Residues: 1-371, M, 373-408, Q', 410-474 < MEA>
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R;Ono, T.; Slaughter, G.R.; Cook, R.G.; Means, A.R.
J. Biol. Chem. 264, 2081-2087, 1989
A;Title: Molecular cloning sequence and distribution of rat calspermin, a high affini
A;Reference number: A32035; MUID:8912372; PMID:2914893
A;Accession: A32035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L16999; NID:g310086; PIDN:AAA17443.1; PID:g310087
C;Comment: Ca2+/calmodulin-dependent protein kinase IV is enriched in cerebellar gran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: Ca2+/calmodulin-dependent protein kinase; protein kinase homology
C;Keywords: alternative splicing; ATP; calmodulin binding; phosphotransferase; serine
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A.TILLE: Calspermin is a testis specific calmodulin-binding protein closely related 48. Reference number: A60255; MUID:90144189; PMID:2618865
A.Reference number: A60255
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A; Residues: 47-141, NE', 144-474 < OH1>
A; Residues: 47-141, NE', 144-474 < OH1>
A; Cross-references: GB:M74488; NID:g203219; PIDN:AAA40845.1; PID:g203220
A; Note: this sequence has been revised in reference A41237
A; Note: part of this sequence was confirmed by sequencing of cDNA to mRNA
R; Ohmstede, C.A.; Bland, M.M.; Merrill, B.M.; Sahyoun, N.
Proc. Natl. Acad Sci. U.S.A. 88, 9375, 1991
A; Reference number: A41237
A; Accession: A41237
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A;Residues: 306-371,'M',373-474 <ON1>
A;Cross-references: GB:J04446; NID:9203642; PIDN:AAA40990.1; PID:9203643
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A; Residues: 142-143 < 0.042>
A; Cross-references: Gs.M63334
A; Cross-references: Gs.M63334
A; Note: this is a revision to the sequence from reference R; Ohmstede, C.A.; Jensen, K.F.; Sahyoun, N.E.
A; Diol. Chem. 264, 5866-5875, 1989
A; Title: Ca(2+)/Calmodulin-dependent protein kinase enri A; Reference number: A32865; MUID:89174647; PMID:2538431
A; Accession: A32865
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F;48-57/Region: protein kinase ATP-binding motif
F;30-474/Product: calspermin *status predicted <CSP>
F;318-337/Region: calmodulin binding *tatus predicted
F;71/Active site: Lys *status predicted
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A, Residues: 335-363 <0N2>
A, Note: the amino end of calspermin was blocked
R, Bland, M.M.
Gene 137, 351-352, 1993
A, Title: Identification of alternate 5' untrans)
A, Reference number: I53706; MUID:94131312; PMIDD
A, Accession: I53706
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Query Match
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Matches
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Ca2+/calmodulin-dependent protein kinase IV beta polypeptide - rat
C32+/calmodulin-dependent protein kinase IV beta polypeptide - rat
C; Species: Rattus sp. (rat)
C; Date: 26-Unl-1996 #sequence_revision 26-Jul-1996 #text_change 18-Jun-1999
C; Accession: 155637
R; Sakagami, H; Kondo, H.
Brain Res. Mol. Brain Res. 19, 215-218, 1993
A; Title: Cloning and sequencing of a gene encoding the beta polypeptide of Ca2+/calmodul
A; Reference number: 152637; MUD:94018484; PMID:8412563
A; Accession: 152637
A; Molecule type: mRNA
A; Residues: 1-502 < RES>
A; Cassidues: 1-502 < RES>
A; Residues: 1-503 < RES>
A; Resi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 EGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTA--LHRDIYPS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----EV 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 KKSPAFRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGV 114
                                                                                                                                                                                                                                           115 YTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSK-MEQN 173
                                                                                                                                                                                                                                                                                                                                      309 AQKKLQEFNARRKLKAAVKAVVASSRLGSASSSHTNIQESNKASSEAQPAQDGKDKTDPL 368
                                                                                                                                                                                                           55 KKSPAFRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGV 114
                                                                                                                                           14 CSSVTSSTENLVPDYWIDGSKRDPLSDFFEVESELGRGATSIVYRCKQKGTQKPYALKVL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 CSSWKKOTTNIRKTF-----IFMEV---LGSGAFSEVFLVKORLTGKLFALKCI 54
                                                          Gaps
                                                                                                        --IFMEV---LGSGAFSEVFLVKQRLTGKLFALKCI 54
                                                                                                                                                                                                                                                                                                                                                                                                              174 GIMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEET-ESKLFEKIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEET-ESKLFEKIK
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                                                        47;
     Length 474;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 VSLQIQKNFAKSKWRQAFNA-----AAVVHHMRKLHMNLHSPGVRP---
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 692.5; DB 2;
Pred. No. 1.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62; Mismatches 120;
  Score 692.5; DB 1;
Pred. No. 1.2e-23;
2; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENR-----PPETQASETSRPSSPEI 353
27.6%; Scol
40.8%; Pre-
tive 62;
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Matches 158; Conservative
                                                        Conservative
                                                                                                        9 CSSWKKQTTNIRKTF-
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  Query Match
Best Local Similarity
Matches 158; Conserv
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Advoin-light-chain kinase (EC 2.7.1.117) A - slime mold (Dictyostelium discoideum)
Nilternate names: MCCKA A
C;Species: Dictyostellum discoideum
A;Title: Characterization and bacterial expression of the Dictyostellum myosin light
A;Title: Characterization and bacterial expression of the Dictyostellum myosin light
A;Reference number: A40811; MUID:91340753; PMID:1651931
A;Reference number: A40811; MUID:91340753; PMID:1651931
A;Reference number: A40811
A;Reference number: A51816-13824, 1990
A;Title: Observation and bacterial expression of the Dictyostellum myosin light chain kinase. Purification and characterization.
A;Reference number: A37125; MUID:90337997; PMID:2380188
A;Mitle: Dictyostellum myosin light chain kinase. Purification and characterization.
A;Reference number: A37125; MUID:90337997; PMID:2380188
A;Molecule type: protein
A;Reference number: A37125; MuiD:90337997; PMID:2380188
A;Pethway: cytokinesis; fruiting body formation
A;Reference number: A37125; PMID:90337997; PMID:9090protein; phosphotransfer-C;Superfamily: kinase-related transforming potein; protein kinase AfP-binding motif
E;265/Domain: protein kinase AfP-binding motif
E;37/Active site: Lys stratus predicted
E;37/Active site: Lys active surface and contrast vincound contrast vincound contrast predicted
E;37/Active si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 KPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDF 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
                                                                                                                                                                                                                    EGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTA--LHRDIYPS 290
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                                              DB 1; Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICHLLEKDPNERYTCEKALSHPWIDGNTA 282
                                                                                                                                                                                                                                                                                                                              ENR------9PETQASETSRPSSPEI 353
                                                                                                                                                                                                                                                                                                                                                                                                          ENKMQAGDHEAAKAAADETMKLQSEEV 423
                                                                                                                                                                     291 VSLQIQKNFAKSKWRQAFNA-
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nes 135; Conserv
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Cal-Y-Calmodulin-dependent protein kinase (EC 2.7.1.123) - Emericella nidulans C. Species: Emericella nidulans, Aspergillus nidulans
C; Species: Emericella nidulans, Aspergillus nidulans
C; Species: Emericella nidulans, Aspergillus nidulans
C; Species: O4-Dec:1992 #sequence_revision 04-Dec:1992 #text_change 21-Jul-2000
C; Accession: JN0323
R; Kornstein, L. B.; Gaiso, M. L.; Hammell, R. L.; Bartelt, D. C.
Gene 113, 75-82, 1992
A; Title: Cloning and sequence determination of a CDNA encoding Aspergillus nidulans c
A; Reference number: JN0323; MUID:9225350; PMID:1563634
A; Molecule type: mRNA
A; Residues: 1-414 - KKOR>
A; Cross-references: GB:M74120; NID:92804304; PIDN:AAB97502.1; PID:9168033
C; Comment: This protein has been implicated in cellular signal transduction and cell c; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinase hom: C; Keywords: AFP: calmodulin binding: Phosphotransferase
F; 21-278/Domain: protein kinase AFP-binding mobif
F; 29-37/Region: calmodulin binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 calmodulin kinase i homolog. [imported] - fission yeast (Schizosaccharomyces pombe)
c; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Species: O9-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C; Accession: T50290
R; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
Submitted to the EMBL Data Library, February 2000
A; Reference number: 225054
A; Reference number: 225054
A; Reference number: 225054
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-335 < WOO>
A; Cross-references: EMBL:AL157993; PIDN:CAB76233.1; GSPDB:GN00066; SPDB:SPACUNK12.02c
A; Cross-references: EMBL:AL157993; PIDN:CAB76233.1; GSPDB:GN00066; SPDB:SPACUNK12.02c
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQN--GIMSTACGTPGYVAPEVLAQKP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 KSLYRFGRTLGAGTYG---IVREADCSSGKVAVKIILKRNVRGNERMYYDELDLLQKLNH 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 RKTFIFMEVLGSGAFSEVFLVKQR--LTGKLFALKCIKKSPAFRDSSLENEIAVLKKIKH 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 YSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 HILEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAAAVVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HMRKLHMNLHSPGVRPEVENRPP--ETQASETSRPSSPEITITEAPVL--DHSVALPALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 414;
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38.3%; Pred. No. 6.8e-22;
ive 78; Mismatches 126;
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----GNGE----SGGTKKRSLSKIARGAI 383
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Matches 149;
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                                                                                            Accession: A5036

Calcabolandin-dependent protein kinase (EC 2.7.1.123) IV - human
Calcabolandin-dependence_revision 10-Sep-1999 #text_change 16-Jun-2000
Cancelession: A5036; UZCABI, 133768
Cancelession: A5036; UZCABI, 133768
AACCESSION: A5036; MUDD:94149862; PMID:8107230
AACCESSION: A5036; MUDD:94149862; PMID:8107230
AACCESSION: A5036
AACCESSI
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48.1%; Pred. No. 2.8e-23;
ive 53; Mismatches 87
270
  242 IGKLLVVDVSKRLNATNALNHPWLKSNNS
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C. Accession: T23616
R.Wild, A. Submitted to the EMBL Data Library, March 1996
A. Reference number: 219771
A. Refe
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C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
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      RKEAYGKPVDIWACGVILYILLVGYPPFWDEDQHKLYQQIKAGAYDFPSPEWDTVTPEAK 246
                                                                                                        247 NLINQMLTINPAKRITAHEALKHPWVCQRSTVASMWHRQETVECLKKFNARRKLKGAILT 306
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                                                                 DFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNF-AKSKWRQA---
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S68470
Cd2+Calmodulin-dependent protein kinase (EC 2.7.1.123) II beta-3 - rat
C,2becies: Rattus norvegicus (Norway rat)
C,2becies: Rattus norvegicus (Norway rat)
C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 18-Jun-1999
C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 18-Jun-1999
C,Accession: S68470
R,Urquidi, V.; Ashcroft, S.J.H.
FEBS Lett. 358, 23-26, 1955
A,Title: A novel pancreatic beta-cell isoform of calcium/calmodulin-dependent protein ki
R,Reference number: 153501; MUD: 95121451; PMID: 7821422
A,Rocession: S68470
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                                                                                                                                                                                                                                                                                                                                          DIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVHRDL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                      145 KPENLLYLTPEENSKIMITDFGLSKMEQNG---IMSTACGTPGYVAPEVLAQKPYSKAVD 201
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                                                                                                                                                                                28 VLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPAFRDSSLENEIAVLKKI--KHENIVTLE
                                                                                                                                                                                                                           202 CWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKD
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                                                              Length 335;
                                                                                                                     56; Mismatches 104; Indels
                                                          Score 630; DB 2;
Pred. No. 4.6e-21;
                                                          25.1%; Score 630; 43.6%; Pred. No. 4
A; Introns: 55/2; 73/3; 104/1; 214/2
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Matches 133;
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Search completed: March 14, 2003, 14:10:05 Job time : $21\ \mathrm{secs}$

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GenCore version 5.1.3
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nucleic search, using sw model OM nucleic

March 14, 2003, 14:07:45; Search time 181 Seconds Run on:

(without alignments) 9488.751 Million cell updates/sec

US-09-960-643-1 2447 Title: Perfect score:

Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters: 501302 seqs, 350932545 residues Searched:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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14: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:* Published_Applications_NA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 4, Appli	7	1,	Sequence 1, Appli	Sequence 3, Appli	1,	ý	و		Sequence 1, Appli	Sequence 48, Appl	Sequence 49, Appl	Sequence 50, Appl	Sequence 189, App	Sequence 7777, Ap		Sequence 3, Appli	H	Ĺ,
	ID	US-09-935-464-4	US-09-935-464-2	US-09-935-464-1	US-10-024-036B-1	US-10-024-036B-3	US-09-935-464-7	US-09-835-788A-6	US-09-935-464-46	US-09-935-464-47	US-09-817-181-1	US-09-935-464-48	US-09-935-464-49	US-09-935-464-50	US-09-764-868-189	US-09-796-692-7777	US-09-935-464-6	US-09-797-039-3	US-09-797-039-1	US-10-153-921-1
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æ	Query	70.9	54.7	37.0	20.6	20.5	20.4	20.3	19.6	17.7	17.7	16.9	13.2	13.0	11.9	10.9	10.0	10.0	10.0	10.0
	Score	1734.8	1339.6	905.6	504.6	502.2	499.4	497	479	434.2	432.4	412.6	324.2	319	291	266.2	244.8	243.6	243.6	243.6
	Result No.	1	7	æ	4	Ŋ	9	7	89	6	10	11	12	13	14	c 15	16	17	18	19

Sequence 201, App Sequence 1, Appli Sequence 82, Appl	Sequence o, Appli Sequence 3, Appli Sequence 5, Appli Sequence 4, Appli		Sequence 522, App Sequence 3371, Ap Sequence 502, App	Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli	Sequence 1, Appli Sequence 1, Appli Sequence 177, App Sequence 177, App	Sequence 20, Appl Sequence 6, Appli Sequence 8, Appli Sequence 10, Appl Sequence 210, App
9 US-09-764-868-201 9 US-10-116-332-1 9 US-10-001-835-82	9 US-10-024-U36B-5 10 US-09-992-481-3 10 US-09-992-481-5 9 US-10-024-036B-4)		9 US-10-217-357-3 10 US-09-975-326-3 9 US-09-934-406-3 0 HS-10-217-357-1	10 US-09-975-326-1 9 US-09-934-406-1 10 US-09-731-872-1177	D D
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215.4 172.4 172.4	172.2	168.6 168.6 166.4	166.4 166.4 160.4	152.8 152.8 152.8	152.8 152.8 149	135.6 131.6 131.6 131.6 124.2
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ALIGNMENTS

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Sequence 4, Application US/0993464

Publication No. US20030027153A1

GENERAL INFORMATION

APPLICANT: Meyer, Joanne

APPLICANT: Barrington-Martin,

APPLICANT: Barrington-Martin,

TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA

FILE REFERENCE: 332/14702 US1

CURRENT APPLICATION NUMBER: US/09/935,464

CURRENT APPLICATION NUMBER: US/09/935,464

PRIOR PILING DATE: 2001-00-03

PRIOR PILING DATE: 2001-01-09

NUMBER OF SEQ ID NOS: 90

SSOFTWARE: Patentin version 3.0

LENGTHA: 1738
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99.9%; Pred. No. 0;
live 0; Mismatches
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Matches 1736; Conservative
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                 US-09-935-464-4
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RESULT 1
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352	412	472	532	592 540		712	772	832	892	952	1012 960	1072 1020	1132	1192	1252	1312	1372
TCAAGCATGAAAACATTGTGACCCTGGAGACATCTATGAGAGCACCACCACTACTACC 	TGGTCATGCAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCTGGAGCGGGGTGTCT 	ACACAGAGAAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAATACCTAC	ATGAGAATGGCATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCTTTACCTTACCCCTG	AAGAGAACTCTAAGATCATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGGCA 	TCATGTCCACTGCCTGTGGGACCCCAGGCTACGTGGCTCCAGAAGTGCTGGCCCAGAAAC	CCIACAGCAAGGCIGIGGATIGCIGGICCATCGGCGTCATCACCTACATATIGCICIGIG	GATACCCCCCGTTCTATGAAGAGAGACTCTAAGCTTTTCGAGAAGATCAAGGAGGCT 	ACTATGAGTTTGAGTCTCCATTCTGGGATGACATTTCTGAGTCAGCCAAGGACTTATTT	GCCACTTGCTTGAGAAGGATCCGAACGGGGTACACCTGTGAGAGGCCTTGAGTCATC	CCTGGATTGACGGAAACACGGCCCTCCACCGGGACATCTACCCATCAGTCAG	TCCAGAAGAACTITGCIAAGAGCAAGIGGAGGCAAGCCTICAACGCAGCAGCTGIGGIGC 	ACCACATGAGGAAGCTACACATGAACCTGCACAGCCCGGGGGTCGCCCCAGAGGTGGAGA	ACAGGCCGCCTGAAACTCAAGCCTCAGAAACCTCTAGACCCAGCTCCCCTGAGATCACCA	TCACCGAGGCACCTGTCCTGGACCACAGTGTAGCACTCCCTGCCCTGACCCAATTACCCT	GCCAGCATGGCCGCCGGCCCACTGCCCCTGGTGGCAGGTCCCTCAACTGCCTGGTCAATG	GCTCCCTCCACATCAGCAGCAGCCTGGTGCCCATGCATCAGGGGTCCCTGGCCGCGGGCCIGGCCGCGGCCGCGGCCGCGGCCGCGGCCGCGGCCGCGGCCGCCGCCGGCCGCG	CCTGTGGCTGCTCCAGCTGCCTGAACAFTGGGA
293	353	413	473	533	593	653	713	773	833	893	953	1013 961	1073	1133	1193	1253	1313
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CURRENT APPLICATION NUMBER: US 09/757,300
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR FILLING DATE: 2001-01-09
PRIOR FILLING DATE: 2001-01-09
SOFTWARE: PATENTIN VERSION 3.0
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DB 9; Length 1383;
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                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-09-935-464-2
; Sequence 2, Application US/09935464
; Publication No. US20030027153A1
; GENERAL INFORMATION:
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US-09-935-464-2
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APPLICANT: Meyer, Joanne Applicant: Meyer, Joanne Applicant: Meyer, Joanne Applicant: Barrington-Martin, Rory
APPLICANT: Barker, Alexander
TITLE OF INVENTION: ALEXANDERS SUCH AS SCHIZOPHRENIA
FITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/14702 USI
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-01-09
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Pred. No. 2.7e-247;
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                     Sequence 1, Application US/09935464 Publication No. US20030027153A1 GENERAL INFORMATION:
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Best Local Similarity 98.5%;
Matches 914; Conservative
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SOFTWARE: Patentin version
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TYPE: DNA
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Sequence 1. Application US/10024036B
Publication No. US20030028004A1
GENERAL INFORMATION:
APPLICANT: Bandaru, Rajasekhar
TITLE OF INVENTION: 68730 and 69112, Protein Kinase
TITLE OF INVENTION: Molecules and Uses Therefor
FILE REFERENCE: MOLECULES and Uses Therefor
FILE REFERENCE: MOLECATION NUMBER: US/10/024,036B
CURRENT FILING DATE: 2001-12-17
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO. 1772
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NAME/KEY: unsure
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; Sequence 3, Application US/10024036B
; Publication No. US20030028004Al
; GENERAL INFORMATION:
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ACTCACTCCCACCTCTCAAGCCTCCAACCTCTGGCCAGATTGGGCTCATTAATGTCGTT 2004
     Sequence 7, Application US/09935464 Publication No. US20030027153A1 GENERAL INFORMATION:
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SEQ ID NO 7
LENGTH: 501
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llarity 99.8%;
Conservative
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ORGANISM: Homo sapiens
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US-09-935-464-7
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                                                                                                                                                                       Score 502.2; DB 9; Length 1074;
Pred. No. 3e-133;
0; Mismatches 273; Indels 6;
                                                                                                                                                                                               Indels
APPLICANT: Bandaru, Rajasekhar TTLE OF INVENTION: 6870 and 69112, Protein Kinase TITLE OF INVENTION: Molecules and Uses Therefor FILE REFERENCE: MPI2000-521P1R(M)
CURRENT APPLICATION NUMBER: US/10/024,036B
PRIOR FILING DATE: 2001-12-17
PRIOR FILING DATE: 2000-12-22
                                                                                  NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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llarity 71.3%;
Conservative 0
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Matches 692; Conserv
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APPLICANT: Meyer, Joanne
APPLICANT: Berrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Darker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSY
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/1H702 US1
CURRENT APPLICATION NUMBER: US(99/935,464
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US (99/757,300
PRIOR FILING DATE: 2001-01-09 ö 1764 1884 TTTGCTAAGAGCAAGTGGAGGCAAGCCTTCAACGCAGCAGCTGTGGTGCACCACATGAGG 1023 1585 CACAGGGAGGAAGGCAGAGCAAGTGGAGCAGGGCTTAGCAGGAGCAGTTCTGGCCAGAA 1644 CCTGACCTGCCTGCTCTATGCCCCACACCCTACGTGCCGTGGCTCTGTGCAGTGTACGTA 1824 360 GTGTCACCTTCTCCAAGCAAAGCCATATGGAGCATCTACCCAGACTCCCACTCTGCACAC 1944 840 61 CAGAGGGAGGAAGGCAGAGCAAGTGGAGCAGGGCTTAGCAGGAGCAGTTTCTGGCCAGAA 120 Gaps CGTAGAAGCCTTGTTGAAGCTGTGAGCAGGAGAAGCGGTGCCCACCAGCTTCCAGGTCTC GATAGCTCTCGCCTGGGTCTGTGCTGTTTGTCGTGAAAAGCTTAATGGGCTGGCCAGGCT GGTGACACACCCTCAACAAAACATCCACGAGTCCGTCAGCGCCCAGATCCGGAAAAAC GCACCAGCCTGCTGCCAGCGGGCCAGCCCCTCATAGGAGGCCCCAGGAGCAGCCCCAAGG ö Length 501; Indels Score 499.4; DB 9; Pred. No. 1.2e-132; 0; Mismatches 1;

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APPLICANT: MOSTILIAN MOSTI
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OTHER INFORMATION: n=a or g or c or t/u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 46, Application US/09935464; Publication No. US20030027153A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn version 3.0
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Matches 479; Conserv
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US-09-935-464-46
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US-09-935-464-46
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LENGTH: 480
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421 ACTCACTCCCACCTCTCAAGCCTCCAACCTCTTGGCCAGATTGGGCTCATTAATGTCGTT 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 GAGAATGAGATAGCCGTCCTGAGAAAGATTAAGCATGAAAATATTGTTGCCCTGGAAGAC 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCTATGAGAGCACCACCACTACTACCTGGTCATGCAGCTTGTTTCTGGTGGGGGGCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 497; DB 10; Length 1
Pred. No. 1.2e-131;
0; Mismatches 265; Indels
                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09835788A Patent No. US20020077458A1 GENERAL INFORMATION:
                                                                        2005 GCCTGCCCATCTGCATG 2025
                                                                                                           481 GCCTGCCCATCTGCATGAATG 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 20.3%;
Best Local Similarity 71.6%;
Matches 682; Conservative
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ORGANISM: Homo sapiens
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Batten to US20020142427A1

GENERAL INFORMATION:

APPLICANT: MERKULOV, Gennady et al

APPLICANT: MERKULOV, Gennady et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND ITILE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/817,181

CURRENT FILING DATE: 2001-03-27
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                                            GTGAAATACCTACATGAGAATGGCATCGTCCACAGAGACTTAAAAGCC
                                                          421 GTGAAATACCTACATGAGAATGGCATCGTNCACAGAGACTTAAAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 432.4; DB 10
Pred. No. 3.2e-113;
                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
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73.98;
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                                                                                                                                                                                                                                                                                                 SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
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                                                                                                                    RESULT 10
US-09-817-181-1
                                                                                                                                                                                                                                                                                                                                                                                          US-09-817-181-1
                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                                                                                 NUMBER OF
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                                                                                                                                                                                                                                                                                             Sequence 47, Application US/0993464
Publication No. US20030027153A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mayer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/1H702 US1
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                           CCTGGAAGAAACACACCACCAACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGGAT
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                                                                                                                                  AGCGGGGTGTCTACACAGAGAAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAG
                                                                                                                                                                                           TGAAATACCTACATGAGAATGGCATCGTCCACAGAGACTTAAAAGCCCGAAAACCTGCTTT
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                                                                       CCCACTACTACCTGGTCATGCAGCTTGTTTCTGGTGGGGGAGCTCTTTGACCGGATCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/935,464 CURRENT FILING DATE: 2001-08-23 PRIOR APPLICATION NUMBER: US 09/757,300 PRIOR FILING DATE: 2001-01-09
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SOFTWARE: Patentin version 3.0
SEQ ID NO 47
LENGTH: 467
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OTHER INFORMATION: n=a or
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US-09-935-464-47
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APPLICANT: Meyer, Joanne
APPLICANT: Meyer, Joanne
APPLICANT: Barrington Martin, Rory
APPLICANT: Barrington Martin, Rory
APPLICANT: Parker,
Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYC,
TITLE OF INVENTION: DISORBRES SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/1H702 US/
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION UNDERS: US 09/757,300
PRIOR APPLICATION UNDERS: US 09/757,300
NUMBER OF SEQ ID NOS: 90
                                                                                                                              APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYC
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 322/1H702 US1
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-01-09
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Pred. No. 1.2e-82;
0; Mismatches 4
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; OTHER INFORMATION: n=a or g or c or t/u
US-09-935-464-49
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                                                                         Sequence 49, Application US/09935464 Publication No. US20030027153A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.2%;
98.0%;
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 49
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ORGANISM: Homo sapiens
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US-09-935-464-50
                                                         US-09-935-464-49
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                                                                                                                                                                                                                                                                                                                    APPLICANT: Meyer, Joanne
APPLICANT: Barrington Martin, Rory
APPLICANT: Barrington Martin, Rory
APPLICANT: Barrington Martin, Rory
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIP
FILE REPERENCE: 3322/11702 USJ
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
PRIOR PAPLICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-09
NUMBER OF SEQ ID NOS: 90
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41 CATCCTCAGAAGCTTCAACTCTGGAGGCAATGGGTCGAAAGGAAGAAGATGACTGCAGTT 100
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                                                                                                                                                  NAME/KEY: misc_feature; OTHER INFORMATION: n=a or g or c or t/u
US-09-935-464-48
                                                                                                                                                                                                                                                            Sequence 48, Application US/09935464 Publication No. US20030027153A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn version 3.0
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ORGANISM: Homo sapiens
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SEQ ID NO 48
LENGTH: 470
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US-09-935-464-48
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
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US-09-796-692-7777/c
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                                                                                                                                                                                                                                                                   101 CCTGGAAGAAACAGACCACCAACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGGAT 160
                                                                                                                                                                                                                                                                                     61 CCTGGAAGAAACAGACCACCAACATCCGGAAAAACCTTCATTTTTTATGGAAGTGCTGGGAT 120
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                                                                                                                                                                                              41 CATCCTCAGAAGCTTCAACTCTGGAGGCAATGGGTCGAAAGGAAGAAGAAGATGACTGCAGTT 100
                                                                                                                                                               Gaps
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 189
LENGTH: 476
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                                                                                                                           Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 189, Application US/09764868
Patent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILLS REFRENCE: PTA32
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
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Pred. No. 4.7e-73;
0; Mismatches 5; Indels
                                                                                                                                                             0; Indels
                                                                                                                           13.0%; Score 319; DB 9; 1
100.0%; Pred. No. 3.6e-81;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (59)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-868-189
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Best Local Similarity 97.8%;
Matches 316; Conservative (
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     SOFTWARE: Patentin version 3.0 SEQ ID NO 50
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                                                                                                                                                             Matches 319; Conservative
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ORGANISM: Homo sapiens
                                                                        CRGANISM: Homo sapiens
US-09-935-464-50
                                                                                                                           Query Match
Best Local Similarity
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LOCATION: (59)
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US-09-764-868-189
                                                           TYPE: DNA
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APPLICANT: Adgate, Paul A.
APPLICANT: Adgate, Paul A.
APPLICANT: Adgate, Paul A.
APPLICANT: Adjate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THE:
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
CURRENT PILING DATE: 2001-03-01
PRIOR PELICATION NUMBER: (0/186,126
PRIOR PELICATION NUMBER: (0/186,126
PRIOR PELICATION NUMBER: (0/100,479
PRIOR APPLICATION NUMBER: (0/200,545
PRIOR APPLICATION NUMBER: (0/200,99)
PRIOR PELICATION NUMBER: (0/200,99)
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILIN
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Pred. No. 5.8e-66;
0; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7777, Application US/09796692 Publication No. US20020198362A1 GENERAL INFORMATION: APPLICANT: Gaiger, Alexander
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; OTHER INFORMATION: n=A,T,C or
US-09-796-692-7777
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10.9%;
Best Local Similarity 73.8%;
Matches 350; Conservative
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OTHER INFORMATION: n=A,T,C
NAME/KEY: unsure
LOCATION: (19)
OTHER INFORMATION: n=A,T,C
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      CIGAAGAGAACTCTAAGATCATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATG
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                         TACATGAGAATGGCATCGTCCACAGAGACTTAAAGCCCGGAAAACCTGCTTTACCTTACCC
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Search completed: March 14, 2003, 17:30:10 Job time: 415 secs

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LENGTH: 1282 base pairs
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STRANDEDNESS: single
TOPOLOGY: linear
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LIBRARY: PROSNOT06
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1 tggagtgggagctcaagcag......tttttctctaaaaaaaaa 2447
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Sequence 1,
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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                    GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-459-448A-20
US-08-459-595R-20
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US-08-905-23-89
US-09-734-030-1
US-08-715-568A-2
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US-09-257-825B-10
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length: 2000000000
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TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
                                      US-09-257-825B-1
US-09-257-825B-1
US-08-459-594A-26
US-08-459-504B-26
US-08-459-444-26
US-09-5444-26
US-09-547-802-36
US-09-467-082-3
US-09-347-801-3
US-09-930-181-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
             -08-655-352-1
-09-258-016-1
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US-09-091-058-1
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PRIOR APPLICATION DATA:
PAPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Bilings, Lucy J
REGISTRATION NUMBER: 36,749
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/08878989
Patent No. 5885803
GENERAL INFORMATION:
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
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MEDIUM TYPE: Diskett
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Matches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225
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                                                                                                                                                                     272 TGCCTTCTCCGAGGTGCTGGCCCCAGGAGCGGGGCTCCGCACACCTCGTGGCCCTCAA 331
                                                                                                                                                                                                                                                               282 GTTGAAAAAGATCAAGCATGAAAACATTGTGACCCTGGAGGACATCTATGAGAGCACCAC 341
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                                                                     Gaps
                                                                                              105 GAAGAAACAGACCACCAACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGGATCAGG 164
                                                                                                              225 GTGCAT --- CAAGAAGTCACCTGCCTTCCGGGACAGCAGCCTGGAGAATGAGATTGCTGT
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                                                                     3;
                                          Length 1282;
                                                                     Indels
                                        Score 418; DB 2; I
Pred. No. 2.8e-109;
0; Mismatches 326;
                                        Query Match
Best Local Similarity 65.5%;
Matches 626; Conservative
; CLONE: 827431
US-08-878-989-12
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Pred. No. 2.8e-109;
0; Mismatches 326;
                                                                                                                                                                                    TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                1: Incyte Pharmaceuticals, Inc
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSTEM: DOS
FastSEQ for Windows Version
ICATION DATA:
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APPLICATION NUMBER: US/09/272,796
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Sequence 12, Application US/09272796 Patent No. 6207148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
                                                      Bandman, Olga
Hillman, Jennifer L
Corley, Neil C.
Guegler, Karl G.
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REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1282 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ilarity 65.5%;
Conservative (
                                                                                        APPLICANT: COTIEY, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                       COUNTRY
ZIP: 94304
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: PROSNOT06
                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                     Palo Alto
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                                       GENERAL INFORMATION:
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IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                ADDRESSEE:
                                                      APPLICANT:
APPLICANT:
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                 511
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                                                                                                                              GGCCCAGAAACCCTACAAGGCTGTGGATTGCTGGTCCATCGGCGTCATCACCTACAT 701
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522 CCTTACCCCTGAAGAGAACTCTAAGATCATGATCACTGACTTTGGTCTGTCCAAGATGGA
                                                             882 CTTGAGTCATCCCTGGATTGACGGAAACACGGCCCTCCACCGGGACATCTACCCATCAGT
                                                                                                                                                                                                                                582 ACAGAATGGCATCATGTCCACTGCCTGTGGGACCCCCAGGCTACGTGGCTCCAGAAGTGCT
                                                                                                                                                                                                                                                                                                                                                                          GCGGGGTGTCTACACAGAGAAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAGT
                                                                                                       162 GAAATACCTACATGAGAATGGCATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 89, Application US/08905223
Patent No. 6222029
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Duelert, Aymerical APPLICANT: Lacroix, Bruno TITLE OF INVENTION: 5' ESTS NUMBER OF SEQUENCES: 503 CORRESPONDENCE ADDRESS:
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STREET: 501 West Broadway
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COMPUTER READABLE FORM:
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STATE: California
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APPLICANT: WEI, Ming-Hui
APPLICANT: DIFRANCESCO, Valentina
APPLICANT: YAN, Chunhua
IITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILLE REFERENCE: CLOO00612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAAACATTGTGACCCTGGAGGACATCTATGAGAGCAC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 5.6
OTHER INFORMATION: seq FIFMEVLGSGAFS/EV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/734,030
CURRENT FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/207,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09734030 Patent No. 6461846
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
                                                                                REFERENCE/DOCKET NUMBER:
TELECOMBUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.8%;
99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BEASLEY, Ellen M. APPLICANT: MERKLOV, Gennady APPLICANT: KETCHUM, Karen A.
                                                                                                                                                                                                          LENGTH: 362 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
                                                                                                                                                                                                                                                                                                                                            Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.8
Best Local Similarity 99.7
Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: sig_peptide
                                                                                                                                                                                                                                                                                                                                                                  TISSUE TYPE: Brain
                                                                                                                                                                                                                                                                                                   CDNA
                                                                                                                                                                                                                                                                             LINEAR
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                                                                                                                                                                                                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   us-08-905-223-89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1030 CGGATCACTGCAGAAGAGGCCATCTCCCATGAGTGGATTTCTGGCAATGCTGCTTCTGAT 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                       645
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                                                                                                                                                                                                                           229 ATCAAGAAGTCACCTGCCTTCCGGGACAGCCTGG---AGAATGAGATTGCTGTTG 285
                                                                                                                                                                                                                                           286 AAAAAGATCAAGCATGAAAACATTGTGACCCTGGAGGACATCTATGAGAGCACCACCAC
                                                                                                                                                                                                                                                                                               526 ACCCCTGAAGAGACTCTAAGATCATGATCACTGACTTTGGTCTGTCCAAGATGGAACAG 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGAAACCCTACAGCAAGGCTGTGGATTGCTGGTCCATCGGCGTCATCACCTACATATTG 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     922 CGGGACATCTACCCATCAGTCAGCCTCCAGATCCAGAAGAACTTTGCTAAGAGCAAGTGG 981
                                                                                                                                                                                                                                                                                                                                 346 TACTACCTGGTCATGCAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCTGGAGCGG 405
                                                                                                                                                                                                                                                                                                                                                                                     GGTGTCTACACAGAGAAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAA 465
                                                                                                                                                                                                                                                                                                                                                                                                              553 GGCTACTACTCGGAGCGAGCACACAAGCAACGTGGTACGGCAAGTCCTGGAGGCCGTGGCC 612
                                                                                                                                                                                                                                                                                                                                                                                                                                        TACCTACATGAGAATGGCATCGTCCACAGAGACTTAAAAGCCCGAAAACCTGCTTTACCTT 525
                                                                                                                                                                       169 TTCTCAGAAGTTTTCCTGGTGAAGCAAAGACTGACTGGGAAGCTCTTTGCTCTGAAGTGC 228
                                                                                                                                                                                                                                                                                                                                               586 AATGGCATCATGTCCACTGCCTGTGGGACCCCCAGGCTACGTGGCTCCAGAAGTGCTGGCC
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                                                                                                                     Length 3124;
                                                                                                                   Score 243.6; DB 4;
Pred. No. 2.6e-59;
0; Mismatches 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     706 CTCTGTGGATACCCCCGTTCTATGAAGAAACGGAGTCT---
                          4.0
           NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
LENGTH: 3124
                                                                                                                    10.0%;
58.5%;
PRIOR FILING DATE: 2000-05-30
                                                                                                                    Query Match 10.0
Best Local Similarity 58.5
Matches 498; Conservative
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                                                               TYPE: DNA ORGANISM: HUMAN
                                                                                          US-09-734-030-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 ITAIGGAAGIGCIGGGAICAGGAGCTIICICAGAAGITIICCIGGIGAAGCAAAGACIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACATCTATGAGAGCACCACCACTACTACCTGGTCATGCAGCTTGTTTCTGGTGGGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 CTGGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCACCTGCCTTCCGGGACAGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGAGAATGAGATTGCTGTGTTGAAAAAGATCAAGCATGAAAAACATTGTGACCCTGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              503 AGCCCGAAAACCTGCTTTACCTTACCCTGAAGAGAACTCTAAGATCATGATCACGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3471;
                                                                                                                                                                                                    ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik STREET: 600 South Avenue West CITY: Westfield STATE: NJ
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                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/AS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,568A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 197.2; DB 2;
Pred. No. 4.8e-46;
0; Mismatches 348;
                                                        GENERAL INFORMATION:
APPLICANT: Brydz, Hans Peter Blankenborg
APPLICANT: Brede, Gaute
TITLE OF INVENTION: PSKH-1 Ribozymes and Uses
TITLE OF INVENTION: Treatment
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORSK 3.0-002
                 ; Sequence 2, Application US/08715568A; Patent No. 5856463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT IMPORMATION:
NAME: FOLEY, Shawn P.
REFERENCE/DOCKET NUMBE: FORS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       908-654-7866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                             ZIP: 07090-1497
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                           07090-1497
                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
US-08-715-568A-2
US-08-715-568A-2
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762

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643 GCCCAGAAACCCTACAGCAAGGCTGTGGATTGCTGGTCGTCGGCGTCATCACTACATA 702
                                                                                                                                           AGCAGGTCTTGTCGGCAGTGAAATACCTACATGAGAATGGCATCGTCCACAGAGACTTAA 502
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                                                                                                                                                                                                                                                                                                                       GACTITATITGCCACTIGCTTGAGAAGGATCCGAACGAGCGGTACACCTGTGAGAAGGCC 882
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                   AAATGCAAGGGTGCCGCCGTCAAGCTGGCTGATTTTGGCCTAGCCATCGAAGTACAGGGA
                                                                              AAGGAGGCTACTATGAGTTTGAGTCTCCCATTCTGGGATGACATTTCTGAGTCAGCCAAG
                                                               GGCATCATGTCCA-----CTGCCTGTGGGACCCCAGGCTACGTGGCTCCAGAAGTGCTG
                                                                                                                                                                                            TIGCICIGIGGATACCCCCCGTTCTATGAAGAAACGGAGTCTAAGCTTTTCGAGAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: AKIRA, SHIZUO
APPLICANT: KAWAI, TARO
TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
FILE REFERENCE: PH-569
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Pred. No. 1.6e-36;
0; Mismatches 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/159,385
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: JP97/261589
EARLIER FILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09159385 Patent No. 5958748
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ilarity 55.3%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Ver. 2.0
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (94)..(1455)
US-09-159-385-3
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Best Local Simi
Matches 361;
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US-09-159-385-3
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 529
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APPLICANT: YE, Jane et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL001158

CURRENT APPLICATION NUMBER: US/09/800,960

CURRENT FILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEC for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 CTTCTGAAACATCCAAACATCGTGCGCCTCCATGACAGTATTTCTGAAGAAGGGTTTCAC 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACTACAGAGAGAGAGCCAGCCAGCCAGTGTATACATCAGATTCTGGAGAGTGTTAACCAC 490
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                                                                                                                            GCTGGTCCATCGCCGTCATCACCTACATATTGCTCTGTGGATACCCCCCGTTCTATGAAG 733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 ACCAAGAAATTGTCTGCCCGGGATCACCAGAAACTAGAACGTGAGGCTCGGATATGTCGA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 AAGATCAAGCATGAAAACATTGTGACCCTGGAGGACATCTATGAGAGCACCACCACTAC 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACCTGGTCATGCAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCTGGAGCGGGGT 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              409 GICTACACAGAGAAGGAIGCCAGICIGGIGAICCAGCAGGICTIGICGGCAGIGAAATAC 468
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TTGGTCTGTC-----CAAGATGGAACAGAATGGCATCATGTCCACTGTGGGA
                   AAACGGAGTCTAAGCTTTTCGAGAAGATCAAGGAGGGCTACTATGAGTTTGAGTCTCCAT
                                                                                                                                                                                                                                                                                                                     854 CGAACGAGGGGTACACCTGTGAGAAGGCCTTGAGTCATCCCTGGATTGACGGAAACACGG
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Pred. No. 5.2e-38;
0; Mismatches 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09800960
Patent No. 6387677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.9%;
Best Local Similarity 54.2%;
Matches 367; Conservative
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; ORGANISM: Human
US-09-800-960-1
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US-09-800-960-1
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                                                                                                                                                                                                     AGCCCGAAAACCTGCTTTACCCTGAAGAG---AACTCTAAGATCATGACACTG
                   575 ACTICGGCATCGCGCACAAGATCGAGGCGGGGAACGAGTTCAAGAACATCTTCGGCACCC
                                                                                                                                                     635 CGGAGTTTGTGGCCCCCAGAGATTGTGAACTATGAGCCGCTGGGCCTGGAGGCGGAGTATGT
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                                                            ACTITIGGICTGICCAAGAIGGAACAGAAIGGCAICAIGTCCACT - - GCCIGIGGGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09159385
Patent No. 5958748
GENERAL INFORMATION:
APPLICANT: AIRA, SHIZUO
TITLE OF INVENTION:
FILE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
FILE REFERENCE: PH-569
CURRENT APPLICATION NUMBER: US/09/159,385
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: J997-09-26
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                    875 AGGGAGAATGACCATTGCCCAGAGCCTGGAACATTCCTGGATTAAGGGGATC
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Pred. No. 1.3e-31;
0; Mismatches 297;
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Best Local Similarity 53.65
Matches 350; Conservative
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US-09-159-385-4
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US-09-159-385-4
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                              515 AGCCGGAAAACATCATGCTGCTGGACAAGAACGTGCCCAACCCACGAATCAAGCTCATCG
                                                                                                                                       677 GGTCCATCGGCGTCATCACCTACATATTGCTCTGTGGATACCCCCCGTTCTATGAAGAAA
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                                                            ACTITIGGICIGICCAAGAIGGAACAGAAIGGCAICAIGICCACI ---GCCIGIGGGACCC
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APPLICANT: KAMAL, TARO
TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
FILE REFERENCE: 081356/0128
CURRENT APPLICATION NUMBER: US/09/186,277
CURRENT PELLING DATE: 1998-11-05
EARLIER FILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09186277 Patent No. 6171841 GENERAL INFORMATION:
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; LOCATION: (94)..(1455)
US-09-186-277-3
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ORGANISM: Homo sapiens
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CCCCTGAAGAACTCTAAGATCATGACTGACTTTGGTCTGTCCAAGATGGAACAGA
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APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, John L.
APPLICANT: Dawson, John L.
APPLICANT: Dander, Erik M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30B
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APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/07951715A Patent No. 5625136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Koziel, Michael G. APPLICANT: Desai, Nalini M. APPLICANT: Lewis, Kelly S. APPLICANT: Kramer, Vance C. APPLICANT: Warren, Gregory W. APPLICANT: Evola, Stephen V.
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Crossland, Lyle D.
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Merlin, Ellis J.
Launis, Karen L.
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US-07-951-715A-20
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                                                                                             CCCAGAAACCCTACAGCAAGGCTGTGGATTGCTGGTCCATCGGCGTCATCACCTACATAT 703
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                                                                       ATGCCATCATGTCC - - - ACTGCCTGTGGGACCCCAGGCTACGTGGCTCCAGAAGTGCTGG
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APPLICANT: AKIRA, SHIZUO
APPLICANT: KAMAI, TARO
TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
FILE REFERENCE: 081356/0128
CURRENT PAPLICATION NUMBER: 0890/186,277
CURRENT FILING DATE: 1998-11-05
EARLIER APPLICATION NUMBER: 1997-09-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATCHIN VOE: 2.0
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Best Local Similarity 53.6%;
Matches 350; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (10)..(1353)
US-09-186-277-4
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Sequence 20, Application US/08459448A Patent No. 5859336
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MEDIUM TYPE: Floppy disk
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Dunder, Erik M.
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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Matches 312; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10591-9005
                       Patent No. 5859336
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
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HYPOTHETICAL:
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TELEFAX: (
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                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                  /note= "cDNA sequence for maize pollen-specific calcium dependent protein kinase gene as disclosed in Figure 30."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 GGGGCGGGAGCTGCGGGCCATCGTGCAGATCGTGCACCTGCCACTCCATGGGG 212
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                                       S-18805/A/CGC 1577/CIP
                                                                                                                                                                                                                                                                                                                                                                                     Score 135.6; DB 1;
Pred. No. 1.1e-28;
0; Mismatches 294;
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-186
TELECOMMUNICATION INFORMATION:
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                         5.5%;
                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 51.5
Matches 312; Conservative
                                                                                                                                                                                                                                                                                LOCATION: 3.1226
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                   NAME/KEY: CDS
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US-08-459-448A-20
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/note= "cDNA sequence for maize pollen-specific calcium dependent protein kinase gene as disclosed in Figure 30."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
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51.5%; Pred. No. 1.1e-28;
Live 0; Mismatches 294;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Launis, Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
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Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
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Suttie, Janet L.
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                                                                                                                            153 GGCGCCGCGGAGCTGCTGCGCCCATCGTGCAGATCGTGCACACCTGCCACTCCATGGGG
                                                                                                                                                          484 ATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCTTTACCTTACCCCTGAAGAGAACTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
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Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
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Dunder, Erik M.
Pace, Gary M.
Suttie, Janet L.
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CORRESPONDENCE ADDRESS:
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APPLICANT: Koziel
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/note= "cDNA sequence for maize pollen-specific calcium dependent protein kinase gene disclosed in Figure 30."
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                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30
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51.5%; Pred. No. 1.1e-28;
iive 0; Mismatches 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE TO THE TOTAL TOTAL TOTAL TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEPHONE: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                            CLASSIFICATION 800
PRIOR APPLICATION BATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-007-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
                                                                                                                                       SCHETTARAN APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595PFILING DATE: 02-JUN-1995
CLASSIFICATION: 800
                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Pace, Gary M. REGISTRATION NUMBER: 40403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH: 1349 base pairs
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Matches 312; Conservative
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STRANDEDNESS: single
                             COMPUTER READABLE FORM:
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OTHER INFORMATION:
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OTHER INFORMATION:
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10591-9005
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SEQUENCE CHARACTERISTICS:

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                                                                                                                                               724 TTCTATGAAGAAACGGAGTCTAAGCTTTTCGAGAAGATCAAGGAGGGCTACTATGAGTTT 783
                     453 TTCTGGGCAGAGAACGAGAACGCATCTTCACCGCCATCCTGCGAGGCAGCTTGACCTC
                                                                               784 GAGTCTCCATTCTGGGATGACATTTCTGAGTCAGCCAAGGACTTTATTTGCCACTTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Pace, Gary M. APPLICANT: Suttle, Janet L. TITLE OF INVENTION: SYMPHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE NUMBER OF SEQUENCES: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
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REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CG1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: No. 6075185artis Corporation
: 3054 Cornwallis Road
Research Triangle Park
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-5UN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-5EP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/08459504B Patent No. 6075185 GENERAL INFORMATION: APPLICANT: Koziel, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rothstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
                                                                                                                                                                                                                                                                                                                                                               Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
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COMPUTER READABLE FORM:
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US-08-459-504B-20
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/note= "cDNA sequence for maize pollen-specific calcium dependent protein kinase gene as disclosed in Figure 30."
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                                                                                                                                                                                                                                                                          Length 1349;
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Pred. No. 1.1e-28;
0; Mismatches 294;
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US-08-459-444-20
S-08-459-444-20
Sequence 0, Application US/08459444A
Patent No. 6121014
GENERAL INFORMATION:
PERICANT: Koziel, Michael G.
Desal, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
                                                                                                                                                                                                                                                                          5.5%;
51.5%;
1349 base pairs
                                                                                                                                                                                                                                                                                           Best Local Similarity 51.5
Matches 312; Conservative
                nucleic acid
                                                                                                                                                                                            OTHER INFORMATION:
OTHER INFORMATION:
US-08-459-504B-20
                                                                            CDNA
                                                                                                                                                      LOCATION: 3..1226
OTHER INFORMATION:
                                                       linear
                                                                        MOLECULE TYPE: CDN
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
                TYPE: nucleic STRANDEDNESS:
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                                                       TOPOLOGY:
LENGTH:
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784 GAGTCTCCATTCTGGGATGACATTTCTGAGTCAGGCCAAGGACTTTATTTGCCACTTGCTT 843
                                                                                                                                             664 GCTGTGGATTGCTGGTCCATCGGCGTCATCATCCTACATATTGCTCTGTGGATACCCCCCG 723
                                                                                                                                                                                                                   TICTATGAAGAAACGGAGTCTAAGCTTTTCGAGAAGATCAAGGAGGCCTACTATGAGTTT 783
544 AAGATCATGATCACCACTTTGGTCTGTCCAAGATGGAACAGAATGGCATCATGTCCACT 603
                                                                       604 GCCTGTGGGGACCCCAGGCTACGTGGCTCCAGAAGTGCTGGCCCAGAAACCCTACAGCAAG
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Job time : 102 secs
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                                                                                                                                                                                   Inc.
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                                                                                                                                                                               ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research,
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
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                                                                                                           INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED NUCLEIC ACID CODING SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 135.6; DB 3; Length 1349;
Pred. No. 1.1e-28;
0; Mismatches 294; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMUTCATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <UNKnOwn>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-0CT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                  Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1349 base pairs
                                                                                          Launis, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 51.5%;
Matches 312; Conservative
                                                                                                                                                              CORRESPONDENCE ADDRESS
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                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                      STATE: NC
COUNTRY: USA
                                                                                                                                                                                                                                                                      ZIP: 27709
                                                                                                           TITLE OF
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Sequence 19, Application US/08878989
Patent No. 5885803
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Rail G.
APPLICANT: Gall, Preeti
APPLICANT: Gall, Preeti
APPLICANT: Shah, Puryl
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATORNEY/GENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER:
REGISTRATION NUMBER:
ATORNEY/GENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER:
REGISTRATION
US-08-459-444-25
US-09-347-402-25
US-09-347-801-17
US-08-464-164-2
US-08-668-416-2
US-09-257-825B-2
US-09-257-825B-2
US-09-159-385-1
US-09-142-551A-2
US-09-142-551A-2
US-09-143-551A-2
US-09-186-277-1
US-09-186-277-1
US-09-186-277-1
US-09-186-277-2
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US-09-186-277-2
US-09-186-277-2
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US-07-857-224B-23
US-09-347-801-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
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SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskette
             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                   March 14, 2003, 14:07:56 ; Search time 16 Seconds
   (without alignments)
   875.332 Million cell updates/sec
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Sequence 14, Api
Sequence 4, Api
Sequence 18, A
Sequence 2, Api
Sequence 2, Api
Sequence 2, Api
Sequence 23, A sequence 23, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2513
1 MGRKEEDDCSSWKKQTTNIR.....VKASGSSHCRAGQTGVCLIM 476
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Sequence 5,
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-960-960-2
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TOPOLOGY: linear IMMEDIATE SOURCE:
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US-09-272-796-19
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                                       Length 370;
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APPLICANT: Corley, Neil C.
APPLICANT: Gridey, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
CORRESPONDENCE ADDRESS:
                                       DB 2;
                                     45.9%; Score 1152.5; DB illarity 55.8%; Pred. No. 1.5e-93; Conservative 46; Mismatches 62
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3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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                                        Query Match
Best Local Similarity
Matches 239; Conserv
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Fatent No. 6387641
GRNERAL INFORMATION:
APPLICANT: Bellon, Steve
TILLE OF INVENTION: Crystallized P38 Complexes
FILE REPERENCE: VPI/98 14
CURRENT APPLICATON NUMBER: US/09/457,040B
CURRENT FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
SEQ ID NO 31
LENGTH: 370
                                                                                                                                                                                                                                                                                                                                                                                                                                 45.9%; Score 1152.5; DB 55.8%; Pred. No. 1.5e-93 tive 46; Mismatches 6
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                                                                   PF-0321
                NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 370 amino acids TYPE: amino acid STRANDEDNESS: single
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 55.8%
Matches 239; Conservative
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           370 LTQLPCQHGRRPTAPGGRSLNCLVNGSLHISSSLVPMHQGSLAAGPCGCCSSCLNIGSKG 429
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      325 -----QEGOGOTASHGELLTPVAGGP-----354
                                                                                                                 12 WKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPAFRDSSLENEIA 70
                                                                        81;
                                            DB 4; Length 370;
                                                                     62; Indels
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APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preetl
APPLICANT: Goli, Preetl
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 21
                                                        ; Pred. No. 1.5e-93; 46; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS SOFTWARE: FASTSED for Windows Version 2.0 CURRENT APPLICATION DATA:
                                           45.9%; Score 1152.5;
55.8%; Pred. No. 1.5e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08878989 Patent No. 5885803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                               ATAVVRHMRKLQLG------
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                     Best Local Similarity 55.89
Matches 239; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  430 KSSYCSEP 437
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ORGANISM: Human
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             US-09-457-040B-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-878-989-5
                                           Query Match
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185 EQKPYGKAVDVWALGVISYILLCGYPPFYDESDPELFSQILRASYEFDXPFWDDISESGK 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 KYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: COLLEY, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goll, Surya K.
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                              39.4%; Score 990; DB 2; 59.8%; Pred. No. 2.9e-79; iive 49; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                   REFERENCE/DOCKET NUMBER: PF-0321 US TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09272796 Patent No. 6207148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                               LENGTH: 343 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 59.89
Matches 193; Conservative
                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                         TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MMEDIATE SOURCE:
LIBRARY: PROSNOT06
ULONE: 827431
                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
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353 ITITEAPVLDHSVALPALTQLPCQHGRRPTAPGGRSLNCLVNGSL--HISSSLVPMHQGS 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 VLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETE-----SKLFEKIKEGYYEFESP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKWRQAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPETQAS--ETSRP-----SSPE 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 AKWKKAVRVTTLMKRLR------APEQSSTAAAQSASATDTATPGAAGGATAAAA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGATSAPEGDAARAAKSDNVAPADRSATPATDG--SATPATDGSVTPATDGSITPATDGS 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 AVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 FWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAK 301
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                                                                                                                                                                                                                                                                     61; Gaps
                                                                                                                                                                                                                                                                                                           15 QTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRD-----SSLENEI 69
                                                                                                                                                                                                                                                                                                                               Length 501;
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STREET: 600 South Avenue West
CITY: Westfield
                                                                                                                                                                                                                                                                     Indels
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Patent No. 5856463
GENERAL INFORMATION:
APPLICANT: Prydz, Hans Peter Blankenborg
APPLICANT: Brede, Gaute
TITLE OF INVENTION: PSKH-1 Ribozymes and Uses in NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                             Ouery Match 29.7%; Score 747.5; DB 4; Best Local Similarity 35.3%; Pred. No. 1.2e-57; Matches 173; Conservative 86; Mismatches 170;
CURRENT APPLICATION NUMBER: US/09/734,030
CURRENT FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/207,281
PRIOR FILING DATE: 2000-05-30
                                                                           NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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                                                                                                               SEQ ID NO 2
LENGTH: 501
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                                                                                                                                                                         ; ORGANISM: HI
US-09-734-030-2
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                                                                                                                                                     TYPE: PRT
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Sequence 2, Application US/09734030

Patent No. 6461846

GENERAL INFORMATION:
APPLICANT: BEASLEY, Ellen M.
APPLICANT: MERKLOV, Gennady
APPLICANT: WIL, Ming-Hui
APPLICANT: WIL, Ming-Hui
APPLICANT: VAN, Chunhua
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 KYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVL 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 KKQTTUIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPAFRDSSLENEIAV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 KKHTEDISSVYEIRERLGSGAFSEVVLAQERGSAHLVALKCIPKKALRGKEALVENEIAV 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.4%; Score 990; DB 4;
59.8%; Pred. No. 2.9e-79;
tive 49; Mismatches 73
                                 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
                                                                                                                                                                                                                                                     ΩS
                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PF-0321
TELECOMNUMICATION HYPORMATION:
TELEPHONE: 415-855-0555
TELEPAS: 415-845-4166
                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 LFLRHIRKL-----GOIPEGE 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 AVVHHMRKLHMNLHSPGVRPEVE 334
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 343 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LIBRARY: PROSI
; CLONE: 827431
US-09-272-796-5
                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Simi
Matches 193;
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Sequence 4, Application US/09800960

Patent No. 6387677

GENERAL INFORMATION:

APPLICANT: FE. Jane et al.

TITLE OF INVENTION: ISOLAFED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

FILE REPERBACE: CL001158

CURRENT APPLICATION NUMBER: US/09/800,960

CURRENT FILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastsEQ for Windows Version 4.0

SEQ ID NO 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 ESTTHYYLVMQLVSGGELFDRILERG-VYTEKDASLVIQQVLSAVKYLHENGIVHRDLKP 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENLLYLTPEENSKIMITDFGLSKMEQNG---IMSTACGTPGYVAPEVLAQKPYSKAVDCW 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDPN 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 LIGRGSFSRVVRVEHRATRQPYAIKMIETKYREGREVCESELRVLRRVRHANIIQLVEVF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 VLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRDSSLENEIAVLKKIKHENIVTLEDIY 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.9%; Score 625; DB 2; Length 26
46.9%; Pred. No. 3e-47;
Live 50; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 592; DB 4;
Pred. No. 7.5e-44;
                           TELEPHONE: (International) 41 1 632 2830 TELEFAX: (International) 41 1 262 2437
                                                                                                                                                                                                                                                         FEATURE: Protein kinase; Table 8 Column 26 PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                               AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein Kinase family JOHNAL: Science
VOLUME: 241
PAGES: 42-52
             TELECOMMUNICATION INFORMATION:
                                                                                     24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 46.99
Matches 119; Conservative
                                                               TELEX: none
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 264
                                                                                                                                                                             MOLECULE TYPE:
DESCRIPTION: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | :|| |||:
248 ARMTALQALRHPWV 261
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                                                                                                                                           amino acid
                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human
                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-857-224B-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-800-960-4
                                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 ENLLYLTPEENSKIMITDFGLSKMEQNG---IMSTACGTPGYVAPEVLAQKPYSKAVDCW 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDPN 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 ERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAAAVVHHMRKLHMN 323
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 EVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRDSSLENEIAVLKKIKHENIVTLEDI 86
                                                                                                                                                                                                                                                                                                                                                                                                               35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INFURION: Predicting Folded Structures of Proteins NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                         Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                               98; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,568A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FOLEY, Shawn P.
REFERENCE/DOCKET NUMBER: FORSK 3.0-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-7866
SINEORATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                     25.9%; Score 650.5; DB 2;
40.2%; Pred. No. 3.5e-49;
tive 62; Mismatches 98;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 LHSPGVRPEVENRPPETQASETSRPS 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371 I-SONLLKRASSRCQSTKSAQSTRSS 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MacIntosh 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
CITY: Zurlch
CITY: Zurlch
STATE: none
COUNTRY: Switzerland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA: none
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OPERATING SYSTEM: MacInto
                                                                                                                                                                                                                                               Best Local Similarity 40.2 Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-07-857-224B-24
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FEATURE: Protein kinase; Table 8 Column
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                                                                                                                                                                                                                                                                                                                                                                             ----- 340
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                                                                                                                                                                                                                                                                                                                                                                                                                              68 LKHPNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCIHQILESVNHI 127
                                                                                                                                                                                                                      AQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAK 251
                                                                                            IKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYL 134
                                                                                                                                                         HENGIVHRDLKPENLLYLTPEENSKIMITDFGLS---KMEQNGIMSTACGTPGYVAPEVL 191
                                                    17 TNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI--KKSPAFRDSSLENEIAVLKK 74
 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18. Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Hadlaubstrand
CITY: Zurich
STATE: none
COUWTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUPER READABLE FORM:
COMPUPER READABLE FORM:
75; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : (International) 41 1 632 2830 (International) 41 1 262 2437
                                                                                                                                                                                                                                                                                                                                                                             307 TMLVSRNFSAAKSLLNKKSDGGVKPQSNNK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        419 CSSCLNIGSKGKSSYCSEPTLLKKANKKQ 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       401 SSRDRTAPSAGMO---POPSLCSSAMRKQ 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MACIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Steven A. Benner
Hadlaubstrasse 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: none TELECOMMUNICATION INFORMATION:
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 Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DESCRIPTION: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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Matches 149;
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APPLICANT: LUYTEN, Walter H.M.L.
APPLICANT: LUYTEN, Walter H.M.L.
APPLICANT: MCGOMAN, Clare H.
APPLICANT: MCGOMAN, Clare H.
APPLICANT: BLASINA, Alessant.
TTLE OF INVERTION: Human Checkpoint Kinase, hCDS1, Compositions and Methods
FILE REFERENCE: TSRI 649.0
CURRENT APPLICATION NUMBER: US/09/529,093A
CURRENT FILING DATE: 2000-04-07
PRIOR FILING DATE: 1998-10-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                                                                                                                                         DIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVHRDL 144
                                                                                                                                                                                                                                                                                                               27 EVLGSGAFSEVFLVKQRLTGKLFALKCI--KKSPAFRDSSLENEIAVLKKIKHENIVTLE 84
                                                                                                                                                                                                                                                                                                                                              7 EELGKGAFSVVRRCVKVLAGQEYAAKIINTKKLSARDHQKLEREARICKLLKHPNIVRLH
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                                                                                                                                                                                                                                 Length 264;
                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                   DB 2;
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                                                                                                                                                                                                                                 23.4%; Score 587.5; DB 2
46.6%; Pred. No. 6.2e-44;
tive 42; Mismatches 88
                                           AUTHORS: Quinn, a...
AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: GB 9722320.0 PRIOR FILING DATE: 1997-10-22 NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09529093A Patent No. 6413755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNERYTCEKALSHPWIDGNTALHR 285
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| PSKRITAAEALKHPWIS----HR 264
                                                                                                                                                                                                                                   Query Match 23.4% Best Local Similarity 46.6% Matches 123; Conservative
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SEQ ID NO 2
LENGTH: 543
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                                    Hanks, S. K.
Quinn, A. M.
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                       PAGES: 42-52
DATE: 1988
                                                                                                                                                                                              US-07-857-224B-18
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US-09-529-093A-2
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Matches 126;
                                      AUTHORS:
                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                           85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 EVLGSGAFSEVFLVKQRLTGKLFALKCI--KKSPAFRDSSLENEIAVLKKIKHENIVTLE 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 DIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVHRDL
                  Predicting Folded Structures of Proteins
                                                                                                              CITY: Zurich
STATE: none
COUNTRY: Switzerland
COUNTRY: Switzerland
ZIP: (note: Liis is an international post code) CH-8092
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 264;
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45.7%; Pred. No. 7.3e-42;
tive 42; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (International) 41 1 632 2830 TELEFAX: (International) 41 1 262 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: Protein kinase; Table 8 Column PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                              OFERTING SIZEM: MACLINGSH 7.0
SOFTWARE: MICROSOft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS: Hunter, T.
TITLE: The protein kinase family JOURNAL: Science
VOLUME: 241
                                                                                                                                                                                                                                COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
                TITLE OF INVENTION: Predicting
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19:
                                                                                          STREET: Hadlaubstrasse 151
CITY: Zurich
    Benner, Steven A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: none
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS: Hanks, S. K. AUTHORS: Quinn, A. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAGES: 42-52
DATE: 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 117;
    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
TYPE: am
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262
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                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09800960
Fatent No. 6387677
GENERAL INFORMATION:
APPLICANT: YE, Jan et al.
APPLICANT: YE, Jan Ect al.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/09/800,960
CURRENT APPLICATION NUMBER: US/09/800,960
CURRENT FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                        320 KEATCKLYFYQMLLAVQYLHENGIIHRDLKPENVLLSSQEEDCLIKITDFGHSKILGETS 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | :| :| :| | | | | 306
247 NLINQMLTINPAKRITADQALKHPWVCQRSTVASMMHRQETVECLRKFNARRKLKGAILT 306
                                                                                                                175 IMSTACGTPGYVAPEVLAQ---KPYSKAVDCWSIGVITYILLCGYPPFYE-ETESKLFEK 230
                                                                                                                                    SLQIQKNFAKSKWRQ----AFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETS 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 IMLVSRNFSVGRQSSAPASPASPAGLAGQAAKSLLNKKSDG---GVKKR----KSSSSV 359
264 ADPAL --- NVETEIELLKKLNHPCIIKIKNFFDA - EDYYIVLELMEGGELFDKVVGNKRL 319
                                    TEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSK-MEQNG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 IKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 HENGIVHRDLKPENLLYLTPEENSKIMITDFGLS---KMEQNGIMSTACGTPGYVAPEVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 AQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFICHLLEKDPNERYTCEKALSHPWIDGNTA----LHRDIYPS------V 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 TNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI--KKSPAFRDSSLENEIAVLKK 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 22.7%; Score 571.5; DB 4; Length 5 Best Local Similarity 34.4%; Pred. No. 4.9e-42; Matches 142; Conservative 69; Mismatches 151; Indels
                                                                                                                                                                                                                  231 IKEGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWI 277
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US-07-857-224B-19
; Sequence 19, Application US/07857224B
; Betent No. 5958784
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Human
US-09-800-960-2
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                                      116
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Gaps

RESULT 14 US-07-951-715A-23

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202 CWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKD 261
                                                                                                                                        65 DSISEEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCIHQILESVNHIHQHDIVHRDL 124
                                        145 KPENLLYLTPEENSKIMITDFGLS---KMEQNGIMSTACGTPGYVAPEVLAQKPYSKAVD 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                     244 PAKRITADQALKHPWVCQRSTVASMMHRQETVECLRKFNARRKLKGA 290
                                                                                                                                                                                             262 PNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNF-AKSKWRQA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: US/08/459,448A FILING DATE: 02-JUN-1995 CLASSIFICATION: 800 PRIOR APPLICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 94
CORRESSONDENCE ADDRESSS:
ADDRESSEE: No. 58F9336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Pace, Gary M.
REGISTRATION NUMBER: CGC 1577/CIP/DIV4
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPRAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/08459448A Patent No. 5859336 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rothstein, steven J.
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
Pace, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: FLODPy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
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Warren, Gregory W
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Lewis, Kelly S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10591-9005
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US-08-459-448A-23
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "rat protein kinase II
protein sequence as shown in Figure 32.
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                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-18805/A/CGC 1577/CIP
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41.8%; Pred. No. 9.5e-42;
iive 56; Mismatches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-00T-1991
ATTORNEY/GENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
TELECOMMUICATION:
TELECOMMUICATION:
TELECOMMUICATION:
TELECHONE: (919)541-8615
TELEFAX: (919)541-8699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/07/951,715A FILING DATE: 25-SEP-1992 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIBA-GEIGY Corporation
Sequence 23, Application US/07951715A Patent No. 5625136 GENERAL INFORMATION:
                                                                                                                                  Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
                                                        Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                Dawson, John L.
Dunder, Erik M.
                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY CC
STREET: 7 SKyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 amino acids
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Matches 120; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION:
; OTHER INFORMATION:
US-07-951-715A-23
                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                  APPLICANT
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                                                                                                                                                                  Gaps
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                                                                                       /note= "rat protein kinase II
protein sequence as shown in Figure 32."
                                                                                                                                       Query Match 22.4%; Score 563.5; DB 2; Length 295; Best Local Similarity 41.8%; Pred. No. 9.5e-42; Matches 120; Conservative 56; Mismatches 104; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                          262 PNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNF-AKSKWRQA 307
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: protein
FRATURE:
NAME/KEY: Protein
LOCATION: 1..295
OTHER INFORMATION: prot
US-08-459-448A-23
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Search completed: March 14, 2003, 14:10:30 Job time : 19 secs

Perfect score:

Title:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB seq Maximum DB seq

Database

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063092 rattus norv

063892 rattus sp.

08122 xenopus lae

088856 datcyosteli

091ya2 mus musculu

091y32 arthrobotry

04267 colletotric

096017 neurospora

096017 neurospora

096095 homo sapien

097899 emericalla

09165 plasmodium

09165 plasmodium

09158 caenorhabdi

09158 caenorhabdi

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09154 caenorhabdi

09154 rattus norv

09191 caenorhabdi

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Ogyzh4 homo sapien
000168 drosophila
09495 drosophila
093559 gallus gall
095266 sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhodes S.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
Lumitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
Lumitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
Rhodes S. SIMILARITY EBLONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
RHSPP. 064450; 1A06.
RICEPPO; 1PR001239; EUK_pkinase.
RICEPPO; 1PR001230; PERNJ_aite.
RICEPPO; 1PR001245; Tyr_pkinase.
RICEPPO; 1PR001245; Tyr_pkinase.
RPGONG9; PKINASE.
RPGONG9; PKINASE.
RPCODM; PD0000001; EUK_pkinase; 1.
RPGONG9; SURK; ALMASE_LOW; UKRNOWN_1.
RPROSITE; PS00129; PRENYLATION; UNKNOWN_1.
RPROSITE; PS0011; PROTEIN_KINASE_LOW; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 53.6 kDa protein (Fragment).
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           Q63092
Q9YGM4
Q63892
Q98TZ2
Q98SR6
Q91YA2
Q9HF33
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008767 rattus norv
099789 mus musculu
090ny2 homo sapien
09txj0 caenorhabdi
09uah6 caenorhabdi
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096nx5 homo sapien
095523 homo sapien
                                                                                                         March 14, 2003, 14:06:52 ; Search time 32 Seconds
(without alignments)
3064.951 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
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Q90NY2
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sp_unclassified:*
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Gaps

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Best Local Similarity 100. Matches 476; Conservative

drosophila homo sapien homo sapien

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Q9V3I4 Q8WTT8 Q9BQC9

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           GTPGYVAPEVLAQKPYSKAVDCWSIGVITXILLCGYPPFYEETESKLFEKIKEGYYEFES
                                                                                            SLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTAC
MGRKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAF
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Characterization of the human ortholog of rat Cam Kinase I gamm "Characterization of the human ortholog of rat Cam Kinase I gamming at 132-q41.";

"CamKIQ) at 132-q41.";

CamKIQ) at 132-q41.";

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF428261; AAL28100.1; -..

EMBL; AF428261; AAL28100.1; -..

Interpro; IPR001299; DevLe,pkinase.

R Interpro; IPR001299; Ser_thr_pkinase.

R Interpro; IPR001299; Ser_thr_pkinase.

R PROSITE; PS000001; Buk_pkinase; 1.

R PROSITE; PS000001; Buk_pkinase; 1.

R PROSITE; PS00010; PROTEIN_KINASE_ATP; UNKNOWN_1.

R PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

R ATP-binding; Kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Calcium/calmodulin-dependent protein kinase I gamma
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Q96NX5;
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-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AL023754; CAA19296.1; -.
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                                   Length 476;
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                                                                        Indels
DD0AEAA016E7506E CRC64;
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Primates; Catarrhini; Hominidae;
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1-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WAY-2002 (TrEMBLrel. 20, Last annotation update)
DJ272L16.1 (Rat Ca2+/calmodulin dependent protein k
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Pred. No. 1.9e-178;
                                 9; DB 4;
4.8e-190;
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                                                                      2; Mismatches
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002299; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
PR051TE; S000205; S. TKC; 1.
PR051TE; PS00107; PR0TEIN_KINASE_DOM; 1.
PR051TE; PS001108; PROTEIN_KINASE_DOM; 1.
PR051TE; PS001108; PROTEIN_KINASE_DOM; 1.
ATP-binding; Serine/threonine-protein kinas
                                    Score 2509;
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates;
 53128 MW;
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Best Local Similarity
 476 AA;
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SEQUENCE FROM N.A.
                                                      Similarity
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Matches 474;
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InterPro; IPR001245; Tyr_pkinase.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
BM106NZ3.1 (Novel protein kinase (Ortholog of human dJ272L16.1 and rat Ca2+/calmodulin dependent protein kinase)
(Calcium/calmodulin-dependent protein kinase I gamma) (Hypothetical 53.3 kDa protein).
BM106NZ3.1 OR CAMKIG.
Mus musculus (Mouse).
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                                                             1 MGRKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAF 60
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus
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      Indels
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EMBL; AL365314; CAC41391; -.
EMBL; AR428262; ABL28101.1; -.
EMBL; BC021840; AAH21840.1; -.
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    Mismatches
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INTECPRO; IPR000719; EUK_Pkinase.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR002290; Ser_thr_pkinase.
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Submitted (OCT-2001) to
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Submitted (MAY-2001)
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447;
    Matches
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.6%; Score 2327.5; DB 11; Lengt
92.0%; Pred. No. 1.1e-175;
Live 14; Mismatches 23; Indels
Pfam; PF00069; pkinase; 1.

Prodom; PD000001; Euk_pkinase; 1.

PROSITE; SM00294; PRENYLATION; UNKNOWN 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.

ATP-binding; Kinase; Transferase; Hypothetical protein.

SEQUENCE 477 AA; 53296 MW; 3A61FBDC49A7BB56 CRC64;
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MEDLINE-97228532; PubMed-9074610;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein kinase (Fragment).
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439; Conserv
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Verploegen S., Koenderman L., Coffer P.J.;
"Identification and characterization of CKLik: a novel granulocyte
Ca2+/calmodulin-dependent kinase.";
                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                   ;
0
                                                                                                                                         Query Match
64.1%; Score 1612; DB 11; Length 309;
Best Local Similarity 98.4%; Pred. No. 2.2e-119;
Matches 304; Conservative 4; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1FA184EEFA976FB4 CRC64;
                                                                                                                      309 AA; 35623 MW; 9162487561CF44E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357 AA
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001249; Suk_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
SWART; SW000209; ExTec; 1.
SWART; SW00210; ExTec; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
ATP-binding; Kinase; Transferase.
SEQUENCE 357 AA; 40189 MW; IFA184EEFA99;
InterPro; IPR001245; Tyr_pkinase.
Pfam: PR00069; Pkinase.
PRINTS: PR00109; TYRKINASE.
PRODOM: PD000001; EUK_pkinase; 1.
SMART; SM001220; Z.TKC; I.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
SCATING/threonine-protein kinase.
NON_TER 309 309
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EMBL; AF286366; AAG00534.1;
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Homo sapiens (Human).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GKESSIENEIAVLRKIKHENIVALEDIYESPNHLYLVWQLVSGGELFDRIVEKGFYTEKD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKN 298
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                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                            1 MGRKEEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPA
                                                                                                                                                                                         60 FRDSSLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKD
                                                                                                                                                                                                                                                                                    ASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNG-IMST
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; Pred. No. 3.5e-83;
43; Mismatches 51; Indels 3;
                                              ;;
    Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OI-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to calcium/calmodulin-dependent protein kinase I.
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37889CDA717D3AB2 CRC64;
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Score 1246; DB 4;
Pred. No. 2.3e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374 AA
                          ; Pred. No. 2.3e
40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC014825; AAH14825.1; -. MGD; MGI:2141437; AI505105.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q91YS8 PRELIMINARY; PRT; Q91YS8; (01-DEC-2001 (TrEMBLrel. 19, Created) (01-DEC-2001 (TrEMBLrel. 19, Last sequen-1-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 FAKSKWRQAFNAAAVVHHMRKLHM 322
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    49.68; 73.18;
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Matches 222; Conservative
                                                Conservative
                          Best Local Similarity
Matches 237; Conserv
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Query Match
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                                                                                                                                                                                                                                                                                                                                               Naitor Y., Watanabe T., Yokokura H., Sugita R., Nishio M., Hidaka H.;

"Isoform-specific activation and structure diversity of calmodulin
kinase I. "."

J. Biol. Chem. 272:32704-32708(1997).

C. 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

BRBL; BAD04267; BAA28263.1; -.

RHSSP, 063450; 1AA06.

RICEPPO: IPRO00719; EUK_PKinase.

RICEPPO: IPRO000290; Ser_thr_pkinase.

R PRODOM; PD000001; EUK_PKinase.

R PRODOM; PD000001; EUK_PKinase.

R PRODOM; PS001001; PROTEIN_KINASE_ATF; I.

R PROSITE; PS00110; PROTEIN_KINASE_DOM; I.

R PROSITE; PS00111; PROTEIN_KINASE_DOM; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 AKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFN 309
                                                                             132 KYLHENGIVHRDLKPENLLYLTPEENSKIMJTDFGLSKMEQNGIMSTACGTPGYVAPEVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 AQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAK 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 VKYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPE 188
                                                                                                                                                                                                                                                         Rattus norvegious (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 343 AA; 38438 MW; 994D451D809A9D80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 VLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.6%; Score 1070; DB 11; Length 343; 59.5%; Pred. No. 1.8e-76; ive 55; Mismatches 74; Indels 12
                                                                                                                                                                                                                       01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) cast-/calmodulin-dependent protein kinase I beta 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74;
                                                                                                                                                                                           343 AA.
                                                                                                                                                                                                                 Created)
                                                                                                                                                                                           PRT;
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                                                                                                            310 AAAVVHHMRKLHMNLHSPG 328
                                                                                                                          | ||| ||||| : | | ATAVVRHMRKLQLGTSQEG 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                              TISSUE=BRAIN;
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Matches 207;
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132 KYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVL 191
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dependent protein kinase I isoforms.";
Biochim. Biophys. Acta 1338:8-12(1997).
-- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; D86556; BAA19879.1; --
HSSP; Q63450; 1A06.
InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yokokura H., Terada O., Naito Y., Hidaka H.;
"Isolation and comparison of rat conwas encoding Ca2+/calmodulin-
dependent protein kinase I isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.5%; Score 1068; DB 11; Length 342; 60.1%; Pred. No. 2.6e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prodom; Pro0069; Prinase; 1.
Prodom; Pro00001; Euk_pkinase; 1.
Prodom; Pro00200; Euk_pkinase; 1.
PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
ATP-binding; Serine-threonine-protein kinase; Transferase. SEQUENCE 342 AA; 38463 WW; 546C464913E784A2 CRC64;
312 AVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAP 359
                              SFLRHIRKL-----GOSPEGE----EASROGMTRHSHPGLGTSOSP 341
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Last annotation update)
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                                                                                                                                                                                                                      Created)
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01-MAY-2000 (TrEMBLrel. 13, Created)
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EMBL; U52111; AAF74509.1; -. HSSP; Q63450; 1A06.
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Matches 201; Conservative
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                                                                                                                                                                                                                                                                          -! - SIMILARITY: BELONGS
                                                                                                                                                                                                               Genomics 44:8-14(1997).
                                                                           Homo sapiens (Human)
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SEQUENCE FROM N.A.
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                              NCBI_TaxID=9606;
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01-MAY-2000 (
01-MAY-2000 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                              MEDLINE-20139438; PubMed-10673339;
Gardner H.B., Rajan J.V., Ha S.I., Copeland N.G., Gilbert D.J.,
Jenkins N.A., Marquis S.T., Chodosh L.A.;
"Cloning, Characterization, and Chromosomal Localization of Pnck,
Ca2+/Calmodulin-Dependent Protein Kinase.";
Genomics 63:129-288(2000).
-! SIMILARITY: BELONGS.
EMBL; AB023027; BA87926.1; -.
EMBL; AR1984; AAF29157.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0109; TYRKINASE.
PRODOM; PRO00001; EUK_pkinase; 1.
PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_TF; 1.
ATP-binding; Scrinc-Chrecoine-protein kinase; Transferase.
SEQUENCE 343 AA; 38519 WW; 1B4A28D36E7A936E CRC64;
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
02-MAKI-BETA2 protein (Pregnancy upregulated NoNUBIQUITOUS
CA2+/calmodulin-dependent kinase PNCK).
PNCK OR CAMKIB OR MCAMKI-BETA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFLRHIRKL-----GQSPEGE---EASRQCMTRHSHPGLGTSQSP 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 AVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                          SEQUENCE FROM N.A.

Uded T.: Minami Y.;

"mCANKI-beta2.";

Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.3%; Score 1064; DB 11;
59.2%; Pred. No. 5.4e-76;
ive 55; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 AA.
                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1347357; Pnck.
InterPro; IPR00719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR01245; Tyr_pkinase.
Pfam; PF00069; pkinase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 59.2°
Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                              Q63450; 1A06.
                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                       TISSUE-BRAIN;
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132 KYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVL 191
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                                                                                                                                                                                                                                                                                                          MEDLINE=97432815; PubMed-9286695; Brenner V., Nyakatura G., Rosenthal A., Platzer M.; Gronpact head "Genomic organization of two novel genes on human Xq28: compact head to head arrangement of IDH gamma and TRAP delta is conserved in rat and mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 KKQTTUIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCI-KKSPAFRDSSLENEIAV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 LKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 343 AA; 38500 MW; E954AEE89DE608C9 CRC64;
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Ca2+/Calmodulin-dependent protein kinase I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.7%; Score 1047; DB 4;
60.7%; Pred. No. 1.2e-74;
tive 52; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pfam; PF00069; pkinase; 1.
PrNTAS; PR00109; TYRKIRASE.
Probom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; PS00102; PROPEIN_KINASE_ATP; 1.
PROSITE; PS0011; PROPEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312 AVVHHMRKLHMNLHSPGVRPEVENRPPETQA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFLRHIRKL -----GQIPEGEGASEQGMA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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PRELIMINARY;
                                                                                                                                                        Caenorhabditis elegans.
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        Eto K., Takal
Tokumitsu H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Q9V3I4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
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-!-SIMICARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

FEMBL, AF099924; AAF23187.1; -.

R RSSP; Q64450; 1A06.

InterPro; IPR002290; Ser_thr_pkinase.

InterPro; IPR00139; Ser_thr_pkinase.

Pfam; PF000069; pkinase; 1.

R PROSITE; SM00220; Ser_tk.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.

R PROSITE; PS00107; PROTEIN_KINASE_LOM; 1.

R PROSITE; PS00108; PROTEIN_KINASE_LOM; 1.

R PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

R ATP-binding; Hypothetical protein; Serine/threonine-protein kinase; Transferase.

SEQUENCE 348 AA; 39124 MW; 88525C390B0A709F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQKPY 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKAVDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICH 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAAAVVHH 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                       investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.1%; Score 1008; DB 5; Length 348; 57.3%; Pred. No. 1.5e-71; tive 68; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BRISTOL N2;
Davidson S., O'Neal D.;
"The sequence of C. elegans cosmid K07A9 ";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
  Last annotation update)
                                                                                                                                                                                                     STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
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01-MAR-2002 (TrEMBLrel. 20, La
Hypothetical 39.1 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 185; Conservative
                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston R.;
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Q9UAH6
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LLEKDPNERYTCEKALSHPWIDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFNAAAVVHH 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 HENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYTEKDASLVIQQVLSAVKYLHE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQKPY 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 IREKYDFRDVLGTGAFSKVFLAESKSDAGQMYAVKCIDKKALKGKEESLENEIKVLRKLR 77
                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Ca2+/calmodulin-dependent protein kinase cascade in Caenorhabditis "Ca2+/calmodulin-dependent protein kinase cascade in Caenorhabditis delgans. Implication in transcriptional activation.";
J. Biol. Chem. 274:22556-22562(1899).
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AB021864: BAA82674.1;
-- HSSP; Q63450; 1A06.
InterPro; IPR0020299; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRODOM; PRODOGO; PRINGS; 1.
PRODOM; PRODOGOI; EUK_pkinase; 1.
PROSTIE; PSO0107; PROTEIN, KINASE_ATP; UNKNOWN_1.
PROSITE; PSO0117; PROTEIN, KINASE_DOM; 1.
PROSITE; PSO01018; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Setzine/threonine-protein kinase; Transferase.
SEQUENCE 348 AA; 39066 WW; 24A2633BF4D8BDBO CRC64;
                                                                                                                                                                                                                                                                                                                                              STRAIN-BRISTOL N2;
MEDLINE-99357789; Pubmed-10428833;
Eto K., Takahashi N., Kimura Y., Masuho Y., Arai K., Muramatsu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.0%; Score 1004; DB 5; Length 3 57.3%; Pred. No. 3e-71; Live 67; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09431; 0944D3; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2002 (TrEMBLrel. 20, Last annotation update) camKI protein.
                                                                            Last sequence update)
Last annotation update)
348 AA.
                                                                            01-MAY-2000 (TrEMBLrel. 13, Last sequence u 01-MAR-2002 (TrEMBLrel. 20, Last annotation Ca2+/calmodulin-dependent protein kinase I.
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                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 MRKLHMNLHSPGVRPEVENRPPE 339
                                                   01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 57.3%;
Matches 185; Conservative (
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RA Adams M.D., Celniker S.E., Holt R.M., Hoskins R.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Holt R.M., Hoskins R.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Holt R.M., Hoskins R.A., Galle R.F.,

Gaorge R.A., Lewis S.E., Richards S., Ashburnar M., Henderson S.N.,

RA Ballow M. C.C., Mogras Y.H.C., Blazej R.G., Champe M., Pfelifer B.D.,

RA Ballow M., Deliniker S.E., Hall G., Nelson C.R., Milos G.L.G.,

RA Ballow M. Basal A., Baxedala J., Bayraktarala D., Beasley E.M.,

RA Ballow M.R., Bouck J. Brokstein P., Brottier P.,

RA Ballow M.R., Bouck J., Butler H., Cadieu E. B., Delishakov S.,

RA Ballow M. Cawley S., Dahlke C., Devenport L.B., Devision S.,

RA Capalos B., Delicher A., Dabne B.P., Bhaddari D., Bolishakov S.,

RA Capalos B., Delicher A., Dang Z., Mays A.D., Dew I., Dietz S.M.,

RA Capalos B., Delicher A., Dang Z., Mays A.D., Dew I., Dietz S.M.,

RA Capalos B., Delicher A., Dang Z., Mays A.D., Dew I., Dietz S.M.,

RA Capalos B., Campelista C.C., Ferrarc S., Fleischmann W.,

RA Clodek A. Gong F., Garry N.S., Galbart W.M., Glasser K.,

RA Clodek A., Gong F., Garry N.S., Garry N.S., Gabriellan A., Rangelista C., Rerriera S., Ralb Dur. B.,

Rollow M., Douston K.A., Howland T.J., Hernandez J. Rollow P., Harman B. M., Marser D., Lau Y., Matter B., McIntosh T.C., McLeod M.P., McDery V. Lin X.,

Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.L.,

RA Shale B., McIntosh T.C., McLeod M.P., McEable J.M.,

RA Sha B. N., Pittman G.S., Bungby M., Nelson D.L.,

RA Sha B.C., Stradiling A.C., Stapheron W., Wang A., Mays A., May M., Willow M., Pittman G.S., Bung M., Wangskern D.R., Wang S., Wang A.,

RA Sha B.C., Staden-Kamos I., Simpson M., Skupsk M., Wang S., Noorges E.,

RA Lings R., Wassarman D.A., Weinsteck G.M., Weinstenbach J.,

RA Sha B.C., Staden-Kamos I., Simpson M., Shang S., Wang A.,

RA Sha R., Wassarman D.A., Weinster D., Wang S., Yao Q.A.,

RA Sheng R., Wassarman D.D., Weinster D.,

"The genome sequence of Drosophila melanogaster.",

"The genome sequenc
                                  Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                   Xu X.Z.S., Wes P.D., Chen H., Li H.S., Yu M., Morgan S., Liu Y.,
                                                                                                                                                                                                                                                                                                                           "Retinal targets for calmodulin include proteins implicated in synaptic transmission.",
   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PSOU107; PROTEIN_KINASE_ATP; 1.
PROSITE; PSOU011; PROTEIN_KINASE_DOM; 1.
PROSITE; PSOU108; PROTEIN_KINASE_ST; 1.
ATP-binding; Alternative splicing; Kinase; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSOF, WOLLD THE STANDOLD TO SEE THE STANDOLD TO SEE THE SEE TH
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SM00220; S_TKC; 1.
                                                                                                                                                                                                         TISSUE-RETINA;
MEDLINE-99030403; PubMed-9813038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y17917; CAA76937.1; -.
EMBL; AE003844; AAF59343.1; -.
EMBL; AE003844; AAF59344.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; Q63450; 1A06
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                        Ephydroidea; Dros
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                          Montell C.;
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PENLLYYSPDDDSKIMISDF -> VRQFYLIYIFNDHLALR
KGK (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
BDE60C6C981CFBC4 CRC64;
                                                                                                                                                                                                                    ELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMIT 163
                                                                                                                                                                                                                                                                                                                        164 DFGLSKMEQNGIMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYEET 223
                                                                                                                                                                                                                                                                                                                                                                                     224 ESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTAL 283
                                                                                                                                                                                                                                                                                                                                                                                                      249 DANLFAQILKGDFEFDSPYWDEISESAKHFIKNLMCVTVEKRYTCKQALGHAWISGNEAS 308
                                                                                                                                                                                                   59 AFRDSSLENEIAVLK-------KIKHENIVTLEDIYESTTHYYLVMQLVSGG 103
                                                                         ; Score 957.5; DB 5; Length 405;
; Pred. No. 1.8e-67;
64; Mismatches 70; Indels 19; Gaps
                                                                                                                                                      2 GRK-EEDDCSSWKKQTTNIRKTFIFMEVLGSGAFSEVFLVKQR-LTGKLFALKCI-KKSP 58
                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 54.4 kDa protein.
Hypothetical 54.4 kDa protein.
Hypothetical 54.4 kDa protein.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 747.5; DB 4; Length 501; Pred. No. 9.4e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019563; AAH19256.1; -.
EMBL; BC017363; AAH19256.1; -.
InterPro; IPR0000104; Antifreeze_1.
InterPro; IPR0000104; Antifreeze_1.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001295; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54353 MW; 1D6DBF8ABA0D1D70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                284 HRDIYPSVSLQIQKNFAKSKWRQAFNAAAVVHHMRKLHMNLHS 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 501 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50011; PROTEIN_KINASE_DOM; 1. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00069; Pkinase; 1.
PRINTS; PR00308; ANTIEREEZEI.
PRIDOm; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TYTKC; 1.
                                                 45113 MW;
                                                                            38.1%;
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35.9%;
                                                                                                            Conservative
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501 AA; 5
                                  191
405 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. TISSUE-LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                               3est_Local Sim
Matches 190;
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                                  VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                             Query Match
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ID Q8WTT8
AC Q8WTT8;
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12;
                                                                                                                                                                         351 AGGATAAAASGATSAPEGDAARAAKSDNVAPADRSATPATDGSATPATDGSVTPATDGSI 410
                                                                                                                                                                                                                                                                                           412 AAGPCGCCSSCLN----IGSKGKSSYCSEPTLLKKANKKQNFKSEVMV---PVKASGSSH 464
                                                                                                                                                                                                                                                                                                        130 AVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPE 189
                                                                                                                                   190 VLAQKPYSKAVDCWSIGVITYILLCGYPPFYEETE-----SKLFEKIKEGYYEFESP 241
                                                                                                                                                                                                               SKWRQAFNAAAVVHHMRKLHMNLHSPGVRPEVENRPPETQASETSRPSSPEITITEAPVL 361
                                                                                                                                                                                                                                                      ---DHSVALPALTQLPCQHGRRP----TAPGGRSLNCLVNGSL--HISSSLVPMHQGSL 411
Gaps
                            15 QTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRD----SSLENEI 69
55;
Indels
81; Mismatches 176;
Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                  465 CRAGOTG 471
                                                                                                                                                                                                                                                                                                                                                     471 APEGATG 477
                                                                                                                                                                                                                                                       362
                                                                                                                                                                                                               302
                                                                                                                                                                    Qy
Db
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Db
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Search completed: March 14, 2003, 14:09:39 Job time: 35 secs

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Db 1487 GGTGGGCAGACTGGGGGTGTCTCGTTATGTGATCCCAGGAGCCCATGTGGGTTTTCAGGA 1546	OY 1528 CAATTITCAGGAGACATATICAACTCCTCTGCTCTTCCAAACCTGGTGTTATCCGGCAG 1587	OY 1588 AGGGAGGAAGGCAAGTGGAGCAGGGCTTAGCAGGAGCAGTTCTGGCCAGAAGCA 1647	OY 1648 CCAGCCTGCTGCCAGCGGGGGGGCCCTCATAGGAGGCCCAGGGGGAGCCCCAAGGCGT 1707 DD 1644 TAGGGCTGTTGCTGCCTGGGCAGCACTCACAGGAAGTCCAGAGGAGCCAGCC	OY 1708 AGAAGCCTTGTTGAAGCTGTGAGGAGAAGCGGTGCCCACCAGCT 1754	OY 1755 TCCAGGTCTCCCTGACCTGCTCTATGCCCCACACCTACGTGCCGTGGCTCTGTGC 1814	OY 1815 AGTGTACGTAGATAGCTCTCGCCTGGGTCTGTGTTGTCGTGAAAAGCTTAATGGGC 1874	OY 1875 TGGCCAGGCTGTGTCACCTTCTCCAAGCAAAGCCATATGGAGCATCTACCCAGACTCCCA 1934 11111111111111111111111111111111111	OY 1935 CTCTGCACACTCACCTCCACCTCTCAAGCCTCCAACCTCTTGGCCAGATTGGGCTGAT 1994	OY 1995 TAATGTCGTTGCCTGCCATCTGCATGAATGACAGGCAGCTCCCCATGGTGGTCTGCCTG 2054	OY 2055 TGACCTCTTCAAGTTCTTAATCCTTAACTCCAGGATTACTCCCAAGTGCGCTGAGACCA 2114	OY 2115 GCCAGCACTTCTGGCCTTCTCCCTGCTCAATCTAAAAGCAGTG-CCACACCCTCCA 2173	OY 2174 AAGTGGAATAGAAAGTTCATGAGTAAGGGCTGCAAGGAATTCTTATCCTGGCCACAT 2233 DD 2159 TGGTGGACTAGAGAAAGCTGTGACTATGGACTTGTGGACTTCTCTCTC	OY 2234 GTCCTCCGTGCCACACCCAATGAGTTAACCTTGGAAGTTGACTATTTAATGTCTGCC 2293 DD 2219 ACCTCATATATCCCTAATTAAGGATTCGGGACTATTTCCATGTCATCC 2267	OY 2294 AGGAGTTCTAATCCTGCTCTGTTCCCTTTGAAAGTCCAGCACACCATTCT 2353 DD 2268 AGGTCTCCTGCCTCTGGCTCCTTCCTTGAAAGTCAGGTGCATTGTTCT 2321	OY 2354 TGTCCTTCCCCAGTTTCCTCGCCCTCCAGCTTCATGCTCAGTTGTGTGT-T 2412	Oy 2413 aataaaatggacatattttctctaaaaaaaa 2447 	C market
	5 1	5 1	· -														

HS272L16 by DNA linear PRI 23-NOV-1999 Undan DNA sequence from clone 272L16 on chromosome 1432.1-32.3. Contains the 3' end of the LAMB3 gene for Laminin, Beta 3 (Nicein, Ralinin, BM600) and a novel Rat Ca2+/Calmodulin dependent Protein

RESULT 8
HS272L16
LOCUS
DEFINITION

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Tylife is from the library RPCII constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: PCTPAC2 This sequence was generated from a human chromosome 1 bacterial clone contig constructed in collaboration by the Sanger Centre chromosome 1 mapping group and Brian Schutte, Bryan Bjork, Kevin Coppage and Jeffrey Murray. Department of Pediatrics, University of Iowa, USA. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1.
                                                                                                                                                                                                                                                                                                                                                                   Submitted (27-NOV-1998) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clonerequest@sanger.ac.uk clonerequest@sanger.ac.uk clone 12, 1998 this sequence version replaced gi:3873472. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  only a small overlap as described above.

Hals sequence is the entire insert of clone 272L16. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
Kinase LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D1S491 and a ca repeat polymorphism, complete sequence.
AL023754
AL023754.1 GI:4007152
                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 157875)
Grafham, D.
Direct Submission
                                                                                                                      HTG; BM600; ca repeat polymorphism; Ca2+/Calmodulin dependent
Protein Kinase; D1S491; Kalinin; LAMB3; Laminin Beta 3; Nicein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5972. .6019
/note="MLTIAL repeat: matches 318. .365 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3677. 4074
/note="MERS4B repeat: matches 486. .902 of consensus"
/NOS9. 5338
/note="MLT1A2-internal repeat: matches 358. .1643 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          966. .1078
/note="MLT11 repeat: matches 281. .410 of consensus"
1082. .1506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5339, .5532
/note="AluJo repeat: matches 101, .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1082. 1506

Anote-"MSTD repeat: matches 1. .426 of consensus"
1585. 1875

Anote-"MITIAI repeat: matches 1. .319 of consensus"
1898. .2024
100te-"MITII repeat: matches 58. .203 of consensus"
2347. .2925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5536. 5966
/note="MLT1A1-internal repeat: matches 5. .450 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6020. .6459
/note="LTR7 repeat: matches 1. .450 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .157875
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="q32.1-32.3"
/clone="RP1-272L16"
/clone_lib="RPCI-1"
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31100. 31107

/note="charilela repeat: matches 1125. 1189 of consensus"

31170. 31914

/note="LIMA repeat: matches 5448. .6190 of consensus"

31923. 32141

/note="LIM2 repeat: matches 4317. 4530 of consensus"
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/note="Charliela repeat: matches 1. .1142 of consensus" 39233. 39437

/note="Match: GSS AQ070531"

/106="match: GSS AQ070531"

/1165. 41445

/106="L. Pepat: matches 2180. .2489 of consensus"

/1615. .41810
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//note="Matha repeat: matches 5. .426 of consensus" 32552. .33436
//note="LiM2 repeat: matches 3451. .4317 of consensus" 33437. .33756
//note="LiM2 repeat: matches 1. .309 of consensus" 33757. .33041
//note="LiM2 repeat: matches 761. .3451 of consensus" 33757. .30041
   /note="L2 repeat: matches 2292. .2723 of consensus"
27779. .27820
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29263. .29500
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29036. .29195
                                                                                                                                           /note="21 copies 2 mer ca 100% conserved"
27779. .27818
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Direct Submission

Submitted (15-UUL-1996) Hisayuki Yokokura, Nagoya University School

Submitted (15-UUL-1996) Hisayuki Yokokura, Nagoya University School

of Medicine, Department of Pharmacology; Tsurumai 65, Showa-ku,

Nagoya, Aichi 466, Japan (Tel:052-744-2075, Fax:052-744-2083)

Location/Qualifiers
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
 CAGCTTCCAGGTCTCCCTGACCTGCCTGCTCTATGCCCCACACCCTACGTGCCGTGGCTC 147770
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/note="similar to calcium/calmodulin-dependent protein
kinase I mRNA (124907, L26288)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 GAGCCCCTGCTTCCCAGGCAGCTTCAACTCTGGAGGACATGGGGCGAAAGGAGGAGGAGG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACTGCAGTTCCTGGAAGAACAGACCACCAACATCCGGAAAACCTTCATTTTATGGAA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 GTGCTCGGATCAGGAGCGTTCTCAGAGGTGTTCCTGGTGAAGCAAAGAGTGACTGGGAAA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CICITIGCICIGAAGIGCAICAAGAAGICACCIGCCIICCGGGACAGCAGCCIGGAGAAI 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACCTGCTTTACCTTACCCCTGAAGAGAACTCTAAGATCATGATCACTGACTTTGGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 GAGTCCCTGGCATCCTCAGAAGCTTCAACTCTGGAGGCAATGGGTCGAAAGGAAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    571 TCCAAGATGGAACAGAATGGCATCATGTCCACTGCCTGTGGGACCCCCAGGCTACGTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCAAGATGGAGCAGAATGGAGTCATGTCCACAGCTTGTGGGGACCCCCAGGCTATGTGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 691 ATCACCTACATATTGCTCTGTGGATACCCCCGTTCTATGAAGAAACGGAGTCTAAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGATTGCTGTTGAAAAAAGATCAAGCATGAAAACATTGTGACCCTGGAGGACATCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGAGCACCACCACTACTACCTGGTCATGCAGCTTGTTTCTGGTGGGGAGCTCTTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGTCGGCAGTGAAATACCTACATGAGAATGGCATCGTCCACAGAGACTTAAAGCCCCGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDGNTALHRDIYPSVSLQIQKNFAKSKWRQAFN"
245 c 262 g 230 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 813; DB 10;
Pred. No. 1.1e-213;
0; Mismatches 95;
                   /organism="Rattus norvegicus"/db_xref="taxon:10116"
                                                                                    /tissue_type="brain"
/clone_lib="S. Nakanishi"
/dev_stage="embryo (E18)"
                                                                                                                                                                                                                                                                             /product="Protein Kinase"
/protein_id="BAA19880.1"
/db_xref="G1:2077934"
                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 33.2%;
Best Local Similarity 90.2%;
Matches 870; Conservative
                                                                   /clone="N5"
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Gaps

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2; Indels

Length 1738;

DB 9;

172

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352 300 412 360 472 420 532

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53 CTTCAACTCTGGAGGCAATGGGTCGAAAGGAAGAAGATGACTGCAGTTCCTGGAAGAAAC
                                                                                                                                                                 113 AGACCACCAACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCT
                                                                                                                                                                                                                                CAGAAGTTTTCCTGGTGAAGCAAAGACTGGGAAGCTCTTTGCTCTGAAGTGCATCA
                                                                                                                                                                                                                                                                                                              TCAAGCATGAAAACATTGTGACCCTGGAGGACATCTATGAGAGCACCACCACCACTACTACC
                                                                                                                                                                                                                                                                                                                                                                           473 ATGAGAATGGCATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCTTTACCTTACCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                533 AAGAGAACTCTAAGATCATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  833 GCCACTTGCTTGAGAAGGATCCGAACGAGCGGTACACCTGTGAGAAGGCCTTGAGTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCAGAAGAACTTTGCTAAGAGCAAGTGGAGGCAAGCCTTCAACGCAGCAGCTGTGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           901 TCCAGAAGAACTTTGCTAAGAGCAAGTGGAGGCAAGCCTTCAACGCAGCAGCTGTGGTGC
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                                    Score 1734.8;
Pred. No. 0;
                                                                    0; Mismatches
                                    70.9%;
                                    Query Match 70.9
Best Local Similarity 99.9
Matches 1736; Conservative
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Vrorlgklfalkcirkspaprdssleneiavlkkirhenivtlediyesthyylvw
Olvsggelfprilergvyterdaslylvqovlsavkytheneityrnbulkerbliltpe
Enskimitdfelskwednginstactpgvyapevlaqkpyskavdowsigyityill
CGYPPFYEETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKA
LSHWIDGNTALHRDIYPSYSLOIOKNFAKSKWRQAFNAAAVHHMRKLHMNIHSPGY
RPEVENRPETGASETSRPSSPEITITEAPVLDHSVALPALTQLPCQHGRRFTAPGGR
SLNCLVNGSAHISSSLYPWHQGSLAAGPCGCSSCLNIGSKGKSSYCSEPTLIKKANK
KQNFKSEVMVPVKASGSSHCRAGQTGVCIM"
                                                                                                                                                                                                                                                               at
      PRI 21-APR-1999
similar to
                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1738)
                                                                                                                                                                                                                         This sequence was generated from cDNA clones isolated using sequence from the bacterial clone 272L16 (AL023754) and EST data. The EST sequences listed match this sequence with an identity of least 95% between the coordinates shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST A1215131 from clone IMAGE:1925595"
                                                                                                                                                                                          Submitted (21-APR-1999) E-mail contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                       Further information can be found at http://www.sanger.ac.uk/HGP/Chr1/ Partial, experimentally determined gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(1469. .1550,1553. .1723,1721. .1738)
/note="matches EST R05661 from clone 29500"
1484. .1736
HS272L161 1738 bp mRNA linear Human gene isolated from PAC 272L16, chromosome 1, calcium/calmodulin dependent protein kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=3
/product="hypothetical protein"
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/db_xref="G1:4678722"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               868. 1159
/note="matches EST AA351937"
931. 1355
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                                                                                                                                                                                                                                                                                                                                        Sanger Centre name: dJ272L16.Cl.1
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .1738
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="1q32.1-32.3"
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/note="matches E
764. .843
                                                               AL049688.1 GI:4678721
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/number=11
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1356. .1483
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/number-8
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/number=4
451. .574
/number=5
575. .650
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/number=6
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237. .311
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/number=7
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ROD 07-AUG-2002 complete cds.
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                                                                                                             TCACCGAGGCACCTGTCCTGGACCACAGTGTAGCACTCCCTGCCCTGACCCAATTACCCT
                                                                                                                                                                                                                                                                                                                                      GCTCCCTCCACATCAGCAGCAGCCTGGTGCCATGCATCAGGGGTCCCTGGCCGGCGGGC
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1
1 (bases 1 to 2416)
Strausberg,R.
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Bmall: cgapbs rdmail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
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IVNGSRRISSSLVPMQQGPLATGPCGCSSCLNIGNKGKSSYCSEPTLFRKANKKQNF
KSEWWPPVKAGGSTHCRGGTSCLVM"

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                                                                           Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M..
Richards, S., Gibbs, R.A.
                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be for
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 41 Row: I Column: 13
This clone was selected for full length sequencing because it
passed the following selection criteria: GenomeScan gene
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                 /clone="MGC:30513 IMAGE:4502479"
/tissue_type="Eye, retina, mouse strain C57Bl\6"
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87. .1520
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                                                              Center code: BCM-HGSC
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Matches 1853; Conservative
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### Controlled in dependent protein kinases. ### Control in Minases.	LOCUS HS272 DEFINITION Human	HS272L161 1738 bp mRNA linear PRI 21-APR-1999 Ruman gene isolated from PAC 272L16, chromosome 1, similar to	ORIGIN	Z
Homo sepiens. EMBOTACIA: CARDIAGA CEALIBLE, VETEDERIA; Buteleostomi; Baiet Local Remon sepiens. EMBOTACIA: MELENCA: Chordsta; Cranista, VerteDeria, Buteleostomi; Butcheria; Etheria; Etheria; Charlette; Cardiaga, Homo. IN CARSES 100 1339 Final Contact: humuner/seasoga ac.uk Submitted (21-New) Better followed 17216 (AL027374) and EST data. This sequence was generated from cDM, closes isolared using a fact. This sequence the coordinates shown. This sequence the coordinates shown. Free EST sequence the coordinates service the co	_	ium/calmodulin dependent protein kinases. 9688 9688.1 GI:4678721	Align Pred. Score	No.: 2.33e- No.: 25.33e- No.: 25.33e- No.: 25.33e-
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The EST sequences from the Bacterial Cione 277LIG (MAD2754) and EST data. The EST sequences listed match this sequence with an identity of at purcher information can be found at http://www.snager.ac.uk/dGp/Chr1/ Partial, experimentally determined gene. S		ct Submission 1fted (21-APR-1999) E-mail contact: humquery@sanger.ac.uk sequence was generated from chub chones isolated using	δ δ	1 MetGlyArgLysGluGluAs
Teast '9 No between the coordinates shown.		ence from the bacterial clone 2721.6 (ALO23754) and EST data. EST sequences listed match this sequence with an identity of at	8 8	21 LysThrPheIlePheMetG
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	deter		Qy	41 LysGlnArgLeuThrGlyLy
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Length:
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Alignment Scores: 3.62e-170 Length: 2447 Pred, No.: 2513.00 Matches: 476 Score: 2513.00 Matches: 476 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches; 0 Query Match: 100.00% Indels: 0 DB: 6 Gans: 0	.09-960-643-2 (1-476) x AX399682 (1-2447)	Oy 1 MetGlyargLysGluGluAspAspCysSerSerTrpLysLysGlnThrThrAsnIleArg 20	Oy 21 LysThrPheIlePheMetGluValLeuGlySerGlyAlaPheSerGluValPheLeuVal 40 	Oy 41 LysGlnArgLeuThrGlyLysLeuPhealaLeuLysCysIleLysLysSerProAlaPhe 60 (11111111111111111111111111111111111	Oy 61 ArgAspSerSerLeuGluAsnGluIlealaValLeuLysIysIleLysHisGluAsnIle 80	<pre>Qy 81 ValThrLeuGluAspIleTyrGluSerThrThrHisTyrTyrLeuValMetGlnLeuVal 100</pre>	Oy 101 SerGlyGlyGluLeuPheAspArglleLeuGluArgGlyValTyrThrGluLysAspAla 120 	Oy 121 SerLeuvalileGlnGlnValLeuSeralaValLysTyrLeuHisGluAsnGlyIleVal 140	Oy 141 HishrgaspheulysProGludsnLeubeuTyrLeuThrProGludludsnSerLyslle 160	Oy 161 MetileThrAspPheGlyLeuSerLysWetGluGlnAsnGlyileWetSerThrAlacys 180	Oy 181 GlyThrProGlyTyrValAlaProGluValLeuAlaGlnLysProTyrSerLysAlaVal 200 	Oy 201 AspCySTrpSerlleGlyVallleThrTyrIleLeuLeuCySGlyTyrProProPheTyr 220 111111111111111111111111111111111	Oy 221 GluGluThrGluSerLysLeuPheGluLysIleLysGluGlyTyrTyrGluPheGluSer 240 [111111111111111111111111111111111111	Oy 241 ProphetrpaspaspileSerGluSeralaLysaspPhelleCysHisLeuLeuGluLys 260 [Oy 261 AspProAsnGluArgTyrThrCysGluLysAlaLeuSerHisProTrpIleAspGlyAsn 280	Oy 281 ThralaLeuHisArgAsplleTyrProSerValSerLeuGlnIleGlnLysAsnPheAla 300 [11] [1] [1] [1] [1] [1] [1] [1] [1] [1	Oy 301 LysSerLysTrpArgGlnAlaPheAsnAlaAlaValValHisHisMetArgLysLeu 320
Oy 301 LysSerLysTrpArgGlnAlaPheAsnAlaAlaAlaAlaAlaAlivaHisHisMetArgLysLeu 320	341 GlahlaSerGluThrSerArgProSerSerProGluIleThrSluhlaProVal 3	Db 1038 CARGCTCAGAACCTCTAGACCCCCCTAGATATATATATATATA	Db 1098 CTGGACCACAGTGTAGCACTCCTGACCCAATTACCCTGCCAGCAGCGCGCGG 1157 Qy 381 ProfhralaProGlydlyAagsacLeusscysLeuvalasGlyScrLeusisleser 400	Db 1158 CCCACTGCCCTGGTGCCTCCAACTGCCTGGTCAATGGCTCCCTCC	1218 AGCAGCCTGGTGCCCATGCAGGGGTCCTGGCCGCGGGGCCCTGTG 421 SerCysLeuAsnIleGlySerLysGlyLysSerSerTyrCysSerGluP	Db 1278 AGCTGCCTGAACATTGGGAGCAAAGTCCTCTACTGCTCTGGGCCCACACTCCTC 1337 Oy 441 LysLysAlaAsnLysLysGlnAsnPheLysSerGluValMetValProValLysAlaSer 460 [[[[[[[[[[[[[[[[[[[[[[[[[[[[[[[[[[[Db 1398 GGCAGCTCCCACTGCCGGGCAGACTGGAGTCTGTCTCATTATG 1445 RESULT 2 AX1996R2	LOCUS AX399682 2447 bp DNA linear PAT 06-JUN-2002 DEFINITION Sequence 3 from Patent WO0224947. ACCESSION AX399682 GT:21315455	S	REFERENCE 1 Manualia; Butheria; Primates; Catarrhini; Hominidae; Homo. AUTHORS Delaney,A.D. and Yoganathan; T.C. TITTE Cancer associated protein timeses and their need	JOURNAL PATENT: WO 0224947-A 3 28-MAR-2002; FEATURES KINETEK PHARMACEUTICALS INC (CA); UNIV BRITISH COLUMBIA (CA) FRATURES LOCATION/Qualifiers		/codon_start=1 //codon_start=1 //protein_id="CAD33521.1" //db_xref="de"(CAD33521.1" //tracell=1:0a=1:0a=1:0a=1:0a=1:0a=1:0a=1:0a=1:0a	TGKLPALKGIKKSPAPROSSLENGY ININKI ET MEVLOSGKISGE PLUKQULG TGKLPALKGIKKSPARDSSLENGEAVLKKIKENIYOLEDIYESTTHYILVMQIVSG GELFDRILERGVYTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENILIYILPEENSKI MITDFGLSKRENDGINGTPOPTVARPROPRIJAKOKTSKRAVDOGRIGVITILLGYPP FYRETRESKIREKTKRGYVRERSCRENDINGSKRAVDOGRIGVITILLGYPP	IDGNTALHRDIYPSYSLQIONNFRKSKRRQAFNAAVVHHMRKLHMIHSPGYRPBYE NRPPETQASETSRPSSPEITITEAPVLDHSVALPALTQLPCQHGRRPTAPGGRSLNCI VNGSLHISSSPEITITEAPVLDHSVALNGSKGKSSYCSEPTLLKKANKKQNFR SFVANDVYR ACCSCHPAROOPCIVITAL	BASE COUNT 590 a 707 c 604 g 546 t

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GGTGCCCACCAGCTTCCAGGTCTCCCTGACCTGCCTGCTCTATGCCCCACACCCTACGTG
                                                                                                                                                                                                            ATCCTGGCCACATGTCCTCCGTGCACACCCAATGGAGTTAACCTTGGAAGTTGACTAT
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and the Storest activity, arthritis and inflammation, leukaemias and the Storest activity, arthritis and inflammation, leukaemias and the storest activity.
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Yang Y,
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Drmanac RT;
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Best Local Similarity 99.5%; Pred. No. 0;
Matches 1941; Conservative 0; Mismatches
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Wehrman T,
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Wang Z,.
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Wang J, Y
Zhao QA,
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AGGACATCTATGAGACCACCACCACTACTGGTCATGCAGCTTGTTTC 371	GGAGCTCTTTGACCGGATCCTGGAGCGGGGTGTCTACACAGAAGGATGCCAG 431 	CTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAATACCTACATGAGAATGGCATCGTCCA 491 	agagacttaaagcccgaaaacctgctttaccttacccctgaagagaactctaagatcat 551 	GATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGGCATCATGTCCACTGCCTGTGG 611 	GACCCCAGGTACGTGGCTCCAGAAGTGCTGGCCCAGAAACCCTACAGCAAGGCTGTGGA 671 	TTGCTGGTCCATCGGCGTCATCACCTACATATGCTCTGTGGATACCCCCGTTCTATGA 731	GAAACGGAGTCTAAGCTTTTCGAGAAGATCAAGGGGGCTACTATGAGTTTGAGTCTCC 791 	attctgggatgacatttctgagtcagccaaggactttatttgccacttgatgaagga 851 	CCGAACGAGGGTACACCTGTGAGAGGCCTTGAGTCATCCCTGGATTGACGGAAACAC 911 	GGCCCTCCACCGGGACATCTACCCATCAGTCAGCCTCCAGAAGAAGATTTGCTAA 971 	GAGCAAGTGGAGGCAAGCCTTCAACGGGGGGGGGGCGCACACATGAGGAAGCTACA 1031 	CATGAACCTGCACAGGCGTCGCCCAGAGGTGGAGAACAGGCCGCTGAAACTCA 1091 	AGCCTCAGAAACCTCTAGACCCAGCTCCCCTGAGATCACCATCACCGAGGCACCTGTCT 1151	GGACCACAGTGTAGCACTCCCTGCCCTGACTTACCCTGCCAGCATGGCCGCGGCC 1211 	GCCCTGGTGGCAGTCCCTCAACTGCCTGGTCAATGGCTCCCTCC	CAGCCTGGTGCCCATGCATCAGGGGTCCCTGGGCCCCGGGCCCTGTGCTCCAG 1331	CTGCCTGAACATTGGGAGCAAAGGAAGTCCTCCTACTGCTCTGAGCCCACACTCCTCAA 1391
GACCCTGGAGGACATCTATGAG 	GGTGG GGTGG		agagacttaaagcccgaaaac 	ATCACTGACTTTGGTCTGTCC 	ACCCCAGGCTACGTGGCTCCA 	TGCTGGTCCATCGGCGTCATC	AGAAACGGAGTCTAAGCTTTTC 	ATTCTGGGATGACATTTCTGAC 	TCCGAACGAGCGGTACACCTG1 	GCCCTCCACCGGGACATCTA(BAGCAAGTGGAGGCAAGCCTT 	CATGAACCTGCACAGCCCGGG 	agcctcagaaacctctagacc 	GGACCACAGTGTAGCACTCCC 	CACTGCCCTGGTGGCAGGTC 	CAGCCTGGTGCCCATGCATCA 	CTGCCTGAACATTGGGAGCAA
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                     1867 ATGGGCTGGCCAGGCTGTGTCACCTTCTCCAAGCAAAGCCATATGGAGCATCTACCCAGA 1926
AAAGGCCAACAAAAAACAGAACTTCAAGTCGGAGGTCATGGTACCAGTTAAAGCCAGTGG 1451
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                                                                         IGIGCCTAIGICACIGCAAITIICAGGAGACAIAITCAACICCICTGCTCTTCCAAACCI
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2000US-0552317.
2000US-0598042.
2000US-065312.
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2000US-0662191.
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model Run on:

(without alignments) 3268.144 Million cell updates/sec March 14, 2003, 17:36:01; Search time 328 Seconds

US-09-960-643-2 Perfect score:

1 MGRKEEDDCSSWKKQTTNIR.....VKASGSSHCRAGQTGVCLIM 476

BLOSUM62 Scoring table:

Sequence:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

2185239 seqs, 1125999159 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length; 0 Maximum DB seq length; 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
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-MODEL-frane+plan.model -DEV=Xlh
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-Q-/cgn2_1/USPTO_spool/US09960643/runat_07032003_090517_19867/app_query.fasta_1.647
-Q-/cgn2_1/USPTO_spool/US09960643/runat_07051X=plan.rng -MINMAYCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN-0 -ALIGN=15
-NODEL-LOCAL -OUTPMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-USO9960643_CGGN_1_1_263_Grunat_07032003_090517_19867 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEOFERY -NCG_SCORES=0 -MAIT -LONGIGG -DEV_TIMEOUT=120
-WARN INMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

Database :

N_Geneseq_101002:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

AA160703 standard; cDNA; 1956 AA160703; AA160703

RESULT 1

(first entry) 22-OCT-2001 Human polynucleotide SEQ ID NO 4692.

Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia; ss.

Homo sapiens

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245 CGGGACAGCAGCCTGGAGAATGAGATTGCTGTGTTGAAAAAGATCAAGCATGAAAAACATT 304

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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM36642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral scleensist, and Shy Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, and thrombolytic activity, arthritis and inflammation, leukaemias and consisting the sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                Wang
                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                             Ren F, Wareng J;
                                                                                                                                                                                                                                                                                                             Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                         Liu C, Asundi V, Chen R, Ma Y, (Wang Z, Wehrman T, Xu C, Xue AJ, Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 4692; 10078pp; English.
                                                                                                                                  25-APR-2000; 20000G-0552317.
09-JUL-2000; 20000G-0598042.
19-JUL-2000; 20000G-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-065191.
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
                                                                                  26-DEC-2000; 2000WO-US34263
                                                                                                                  2000US-0488725
                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-442253/47.
P-PSDB; AAM41547.
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              WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specification
                                                                                                                   21-JAN-2000;
                                                26-JUL-2001
                                                                                                                                                                                                                                                                                                         Tang YT,
Wang J, W
Zhao QA,
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SQ Sequence 1956 BP; 474 A; 559 C; 508 G; 414 T; 1 other;
Alignment Scores:
Score:
Score:
Score:
Score:
100.008
Matches:
100.008
Mismatches:
0
DBs:
100.008
Mismatches:
0
DBs:
22
Gaps:
0

US-09-960-643-2 (1-476) x AAI60703 (1-1956)

61 ArgAspSerSerLeuGluAsnGluIleAlaValLeuLysIysIleLysHisGluAsnIle 80

g	b 245 CGGGACAGCAGCCTGGAGA	atgagattgctgtgttgaaaaagatcaagcatgaaaacatt 304
δy	81 ValThrLeuGluAspIleT	yrGluSerThrThrHisTyrTyrLeuValMetGlnLeuVal 100
QQ	305 GTGACCCTGGAGGACATCT	reagageaccaccactactactggtcarccacctrgff 36
Qy	101 SerGlyGlyGluLeuPhe 	AspargIleLeuGluArgGlyValTyrThrGluLysAspala 120
λŏ	121 SerLeuVallleGlnGln	11LeuSerAlaValLysTyrLeuHisGluAsnGlyIleVal 14
qq		
ογ	141 HisargaspLeuLysPrc	UASSILeuLeuTyrLeuThrProGluGluAsnSerLysIle 1
g	485 CACAGAGACTTAAAGCCC	CTGCTTTACCTTACCCCTGAAGAGAACTCTAAGATC 54
δ i	161 MetileThrAspPheGly	SerLysMetGluGlnAsnGlyIleMetSerThrAlaCys 18
සු	545 ATGATCACTGACTTTGGT	rccaagarggaacagaarggcarcargrccacrgccrgr 60
& A	181 GlyThrProGlyTyrVal 	AlabrogiuvailenalaginiysProTyrSeriysAlavai 200
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οy	221 GluGluThrGluS	PheGluLysileLysGluGlyTyrTyrGluPheGluSer 24
q	725 GAAGAAACGGAGTC	
δλ	241 ProPheTrpAspAspIleS	erGluSerAlaLysAspPheIleCysHisLeuLeuGluLys 26
q	785 CCATTCTGGGATGACATTT	CTGAGTCAGCCAAGGACTTTATTTTGCCACTTGCTTGAGAG 84
Qy	261 AspProAsnGluArgTyr	/sGluLysalaLeuSerHisProTrp1leAspGlyAsn 28
q	845 GATCCGAACGAGCGGTAC	TGTGAGAAGGCCTTGACCTCGCTGATTGACGGAAAC 9
δλ	281 ThralaLeuHisArgAsp	**TyrProSerValSerLeuGlnIleGlnLysAsnPheAla 30
q	905 ACAGCCCTCCACCGG	TACCCATCAGTCAGCCTCCAGATCCAGAAGTTTGCT
Qy	301 LysSerLysTrpArgC	eAsnalaalaalaValValHisHisMetArgLysLeu 32
qq	965 AAGAGCAAGTGGAGGG	CAACGCAGCAGCTGTGCTGCACCACATCAGGAAGCTA 10
Qy	321 HisMetAsnLeuHisS	yvalArgProGluValG
qq	1025 CACATGAACCTGCACAGC	SGCSTCCGCCCAGAGGTGGAGAACAGGCCGCCTGAAACT 10
QY	341 GlnAlaSerGluThrSer	Ō
Q	1085 CAAGCCTCAGAAAC	GCTCCCCTGAGATCACCATCACCGAGGCACCTGTC 11
Qy	361 LeuAspHisSerVa	euThrGlnLeuProCysGlnHisGlyArgArg 38
Q	1145 creeaccacaerer	cereacedarracereceaecareeceee
δλ	381 ProThrAlaProGlyGly	AsnCysLeuValAsnGlySerLeuHisIleSer 40
qq	1205 cccacrecccregreec	stoccicaacidecidescandecicciccacaicae
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Alignment Scores:

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Human; cytostatic; antisense gene therapy; screening; protein kinase;
cancer; liver; colon; tumour; inflammation; arthritic synovium; CAMK-X1;
calmodulin kinase; enzyme; gene; chromosome 1q32.1-32.3; ds.
                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing cancer, comprises determining the upregulation of expression of a nucleic acid sequence encoding a protein kinase or upregulation of expression of the protein kinase, in the cancer
Location/Qualifiers
/*tog= a /*tog= a /*toman CAMK-X1 protein"
                                                                                                                              calmodulin kinase, CAMK-X1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 16; Page 62-64; 87pp; English
                                                                                ВÞ
                                                                                                                                                                                                                                                                                                                                   KINETEK PHARM INC.
UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                            2000US-237419P.
2000US-237423P.
2000US-238558P.
2001US-290555P.
                                                                               DNA; 2447
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                                                                                                               (first entry)
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P-PSDB; AAE22764.
                                                                               AAD36140 standard;
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02-0CT-2000;
04-0CT-2000;
10-MAY-2001;
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The invention relates to a method for screening biologically active agent that modulates cancer associated protein kinase function. The invention also relates to a method for diagnosing cancer comprising determining the upregulation of expression of a nucleic acid sequence encoding a protein kinase. The method is useful for diagnosing cancer. A protein kinase is useful for screening biological agents that modulate cancer associated protein kinase function. Downrequlating the activity of protein kinase is useful for inhibiting the growth of a cancer cell, e.g. liver or colon cancer. A nucleic acid encoding protein kinase is useful for inhibiting the growth of a cancer cell, e.g. liver or colon cancer. A nucleic acid encoding protein kinase is useful to screen biopsy derived tumours and inflammatory samples such as arthritic synovium, for amplified DNA in the cell or increased expression of corresponding mRNA or protein and is also useful to detect differences in expression levels such as molecular weight, amino acid and nucleotide sequences between the two cells. The present sequence is human calmodulin kinase CAMK-X1 gene
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T; 0 other;

G; 546

A; 707 C; 604

Seguence 2447 BP; 590

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                                                                                                                                                     ArgAspSerSerLeuGluAsnGluIleAlaValLeuLysLysIleLysHisGluAsnIle
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                                                                                                                                                                                                                                              SerGlyGlyGluLeuPheAspArgIleLeuGluArgGlyValTyrThrGluLysAspAla
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                                                                                                           LysThrPheIlePheMetGluValLeuGlySerGlyAlaPheSerGluValPheLeuVal
                                                                                                                                             LysGlnArgLeuThrGlyLysLeuPheAlaLeuLysCysIleLysLysSerProAlaPhe
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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DB:
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2003, 10:03:49; Search time 566 Seconds
(without alignments)
9736.113 Million cell updates/sec
Title: US-09-960-643-1
Perfect score: 2447

Title: Perfect score: 2447 Sequence: 1 tggagtgggagctcaagcag......ttttctctaaaaaaaaa 2447

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Total number of hits satisfying chosen parameters: 4370478

2185239 seqs, 1125999159 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : N_Geneseq_101002:*

i. N.Geneseq_101002:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Score Match Length DB ID Description

247 100.0 247 24 AAD36440 Human calmodulin k
1915 78.3 1956 22 AAI60703 Human polynuclecti
1964.6 75.8 2165 22 AAI68917 Human polynuclecti
1761.6 72.0 2689 22 AAS31014 Human polynuclecti
504.6 20.6 1565 24 ABL60905 Human CaM kinase I
504.6 20.6 1661 22 AAD18826 Human Cam kinase (PKIN
504.6 20.6 1671 22 AAB158210 Human polynuclectic
504.6 20.6 1671 22 AAB15838 Human polynuclectic
504.6 20.6 1733 22 AAB15838 Human polynuclectic

Human polynucleoti Polynucleotide seq	Nucleotide sequenc	Nucleotide sequenc	Human death domain	Murine Dendritic C	cDNA sequence enco	Calmodulin-depende	Polynucleotide seq		Disease associated	DNA encoding novel	Human secreted pro	cDNA encoding nove	DNA encoding novel	Drosophila melanog		DNA encoding novel	DNA encoding novel	Human protein phos		Human kinase (PKIN	\sim		Human polynucleoti			Human full-length	DNA encoding novel	Human cDNA encodin	cDNA encoding nove	DNA encoding novel	PSKH-1 cDNA. Homo	Human polynucleoti	Human polynucleoti	Human ORFX ORF2112
AA160424 AAS06708	AAH25119	AAH25118	AAD04775	AAC90432	AAZ46162	AAV18867	AAS06711	ABK43480	AAX06835	AAS70157	AAX51838	AAS27154	ABK43797	ABL02719	AAH99632	AAS68767	AAS90919	AAF30481	AAK94325	AAD18832	AAH78261	AAI58143	AAI58144	ABA95682	AAK94614	AAK94299	ABK43538	AAS34308	AAS27166	ABK43848	AAT71761	AAK52586	AAK51602	AAC76557
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503	502.2	502.2	497	492.6	471.4	428.8	427	426.2		393.8	337.2	291	291	290	286.4	285.6	285.6	245.2	245.2	245.2	243.6	243.6	243.6	243.6	242	242	217.8	215.4	215.4	215.4	9	194	194	185.2
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ALIGNMENTS

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Human; cytostatic; antisense gene therapy; screening; protein kinase; cancer; liver; colon; tumour; inflammation; arthritic synovium; CAMK-X1; calmodulin kinase; enzyme; gene; chromosome 1q32.1-32.3; ds.
                                                                                                                                                                                              "Human CAMK-X1 protein"
                                                                               Human calmodulin kinase, CAMK-X1 gene.
                                                                                                                                                              Location/Qualifiers
70..1500
/*tag= a
/product= "Human CAMK
                  AAD36140 standard; DNA; 2447 BP
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2000US-237419P.
2000US-237423P.
2000US-238558P.
2001US-290555P.
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                                                            (first entry)
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02-OCT-2000; 2
02-OCT-2000; 2
04-OCT-2000; 2
10-MAY-2001; 2
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                                        AAD36140;
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RESULT 1
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The invention relates to a method for screening biologically active agent that modulates cancer associated protein kinase function. The invention also relates to a method for diagnosing cancer comprising determining the upregulation of expression of a nucleic acid sequence encoding a protein kinase. The method is useful for diagnosing cancer. A protein kinase is useful for screening biological agents that modulate cancer associated protein kinase function. Downregulating the activity of protein kinase is useful for inhibiting the growth of a cancer cell, e.g. liver or colon cancer. A nucleic acid encoding protein kinase is useful for inhibiting the growth of a cancer cell, e.g. liver or colon cancer. A nucleic acid encoding protein kinase is useful to screen biopsy amplified DNA in the cell or increased expression of corresponding mRNA or protein and is also useful to detect differences in expression levels such as molecular weight, amino acid and nucleotide sequences between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is human calmodulin kinase CAMK-X1 gene
                                                                                                                                                                                                    Diagnosing cancer, comprises determining the upregulation of expression of a nucleic acid sequence encoding a protein kinase or upregulation of expression of the protein kinase, in the cancer
                                                                                                                                                                                                                                                                                             62-64; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          located on chromosome 1q32.1-32.3.
                                            BRITISH COLUMBIA.
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Ouery Match

Best Local Similarity 100.0%; Score 2447; DB 24; Length 2447;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2447; Conservative 0; Mismatches 0; Indels 0; 0

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                         AACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTT
                                                                                              TTCCTGGTGAAGCAAAGACTGACTGGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCA
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CCGTGGCTCTGTGCAGTGTACGTAGATAGCTCTCGCCTGGGTCTGTGCTGTTTGTCGTGA
                                                                                                                     GGTGCCCACCAGCTTCCAGGTCTCCTGACCTGCTCTATGCCCCACACCCTACGTG
                                                                                CCGTGGCTCTGTGCAGTGTACGTAGATAGCTCTCGCCTGGGTCTGTGTGTTTGTCGTGA
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the encoded polypeptides (AAW38642-AAW42213) with nootropic, mamunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous that as a neripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic atteral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic as and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and CNNS disorders
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Drmanac RT;
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Wehrman T,
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Wang Z,
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                                                                                                                                                                                                    the encoded polypeptides (AAMA2113) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as lateral sclerosis, and shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                                               leukaemias and
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                                                Ren F,
Zhang J
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                                                Qian XB,
Yang Y,
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                                               u C, Xue AJ,
Drmanac RT;
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Pred. No. 0;
0; Mismatches
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                                                                                                                                  polypeptides, us
system injuries
                                               Chen R,
Xu C, X
                                               Asundi V, Che
Wehrman T, Xu
Goodrich R,
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Best Local Similarity 98.3%;
Matches 1914; Conservative
29-NOV-2000; 2000US-0727344
                                                                                                                                Novel nucleic acids and
                                                                                                                                             such as central nervous
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                                               Liu C, A
Wang Z, W
Zhou P,
                         HYSEQ INC
                                                                                                           P-PSDB; AAM39761
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TCTGGCCAGAAGCACCAGCCTGCTGCCAGCGGGGCAGCCCCTCATAGGAGGCCCCAGGAGG 1693
                            1838 TCTGGCCAGAAGCACCAGCCTGCTGCCCAGGGGGGCAGCCCCTCATAGGAGGCCCAGAGG 1897
                                                                                                       GAGCCCCAAGGCGTAGAAGCCTTGTTGAAGCTGTGAGCAGGAGAAGCGGTGCCCACCAGC 1753
                                                                                                                                       TTCCAGGTCTCCCTGACCTGCCTGCTCTATGCCCCACACCCTACGTGGCCGTGGCTCTGT 2017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human diagnostic and therapeutic polynucleotide (DITHP) #29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2138 CCCACTCTGNACACACTCACTCCCACCT 2165
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2000US-0184777.
2000US-0184797.
2000US-0184813.
2000US-0184837.
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2000US-0184773.
2000US-0184774.
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2000US-0204908.
2000US-0205232.
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24-FEB-2000;
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The invention relates to polynuclectides (I) encoding diagnostic and therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, and proteins involved in growth and development and receptors. (I) and can proteins involved in growth and development and receptors. (I) and suscitated with inappropriate DITHP expression. For example, (I) and (II) may be used to treat disorders associated with decreased polypeptide carpession by rectifying mutations or deletions in a patient's genome, that affect the activity of the DITHPS, by expressing inactive proteins or supplementing the patient's own production of them. (I) and (II) may be used to treat diseases, for example, cell proliferative disorder. Crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma, leukaemia, autoimmune disorders, and respiratory disorders. Additionally, into a host cell and culturing the cell to express the protein. (I) and its complementary sequences may also be used as DNA probes in diagnostic samples, and therefore which patients may be in need of restorative theresis and therefore which patients may be in need of restorative theresis and activity. The anti-DITHP antibodies and antagonists may also be used as antigens in the production of antibodies against DITHPs and in assays to identify modulators of DITHP expression and activity. The anti-DITHP antibodies may also be used as diagnostic agents for detecting the presence of DITHPP antibodies may also be used as diagnostic agents for detecting the presence of DITHPP antibodies way also be used as diagnostic agents for detecting the presence of DITHPP antibodies way also be used as diagnostic agents for antibodies may also be used as diagnostic agents for antibodies may also be used as diagnostic agents for detecting the presence of DITHPP antibodies way ELISA).

The presence of DITHPP in samples (e.g. by enzyme linked immunosorbant and contractive presence of DITHPP antibodies and diagnostic and diagnostic and diagnostic and diagnostic and diagnostic and diagnostic and dia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones AL;
Daffo A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotides encoding diagnostic and therapeutic proteins, e.g. enzymes, hormones and receptors, useful in diagnostics and therapeutics
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                                                                                                                                                                                                                                                                                                                                                                                                                 Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC; Chen A, D'Sa SA, Amshey S, Dahl CR, Dam TC, Daniels SE; Dufour GE, Flores V, Fong WT, Greenawalt LB, Hillman JL, Jones Liu TF, Roseberry AM, Rosen BH, Russo FD, Stockdreher TK, Daffo Warlght RJ, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen W; Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;
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0; Mismatches 159; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 310-311; 522pp; English.
                            17-MAY-2000; 2000US-0204863.
17-MAY-2000; 2000US-020521.
17-MAY-2000; 2000US-0205285.
17-MAY-2000; 2000US-0205281.
17-MAY-2000; 2000US-0205281.
17-MAY-2000; 2000US-0205323.
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1 00	CTGAAGTGCATCAAGAAGTCACCTGCCTTCCGGGACAGCAGCCTGGAGAATGAGATTGC 44.
279	TGTGTTGAAAAGATCAAGCATGAAAACATTGTGACCCTGGAGGACATCTATGAGAGCAC 338
339	CACCCACTACTACCTGGTCATGCAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCT 398
399	GGAGCGGGTGTCTACACAGAAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGC 458
459	AGTGAAATACCTACATGAGAATGGCATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCT 518
519	TTACCTTACCCCTGAAGAGACTCTAAGATCATGATCACTGACTTTGGTCTGTCCAAGAT 578
579 746	GGAACAGAATGGCATCATGTCCACTGCGCTCTGGGACCCCAGGCTACGTGGCTCCAGAAGT 638
639	GCTGGCCCAGAAACCCTACAGCAAGGCTGTGGATTGCTGGTCCATCGGCGTCATCACCTA 698
998	CATATTGCTCTGTGGATACCCCCCGTTCTATGAACAAACGGAGTCTAAGCTTTTGGAGA 758
759 926	GATCAAGGAGGCTACTATGAGTTTGAGTCTCCATTCTGGGATGACATTTCTGAGTCAGC 818
819 986	CAAGGACTTTATTTGCCACTTGCTTGAGAGGATCCGAACGA-GCGGTACACCTGTGAGA 877
878 1046	AGGCCTTGAGTCATCCCTGGATTGACGGAAACACGGCCCTCCACCGGGACATCTACCCAT 937
938 1106	CAGTCA-GCCTCCAGATCCAGAAGATTTGCTAAGAGCAAGTGGAGGCAAGCCTTCAAC 996
997 1166	GCAGCAGCAGCTGTGGT-GCACCACATGAGGAAGCTACACATGAACCTGCACA-GCCCGGGCG 1054
1055 1226	TCGCCCAGAGGTGGAGAACAGGCCGCCTGAAACTCAAGCCTCAGAACCTCTAGACCCA 1114
1115 1286	GCTCCCCTGAGATCACCATCACCGAGGCACCTGTCCTGGACCACAGTGTAGCACTCCCTG 1174
1175 1346	CCCTGAUCCAATTACCCTGCCAGCATGGCCGCCGCCCCTGCTGCTGGCGGGGT 1231
1232 1406	CCCTCAACTGCCTGGTCAATGGCTCCCTCCACATCAGCAGCCTGGTGCCCATGCATC 1291
1292 1466	AGGGGTCCCTGGCCGCCCCGGGCCCTGTGGCTGCTGCTGCT

GGCTGGCCAGGCTGTGTCACCTTCTCCAAGCAAAGCCATAT---GGAGCATCTACCC--- 1925 1946 TCTCCCGTGACCTGGCCTCTATAGCCCCACACCCTACAGTGGCCGTGGCTCTGTGCAG AAAGGAAAGTCCTCCTACTGCTCTGAGCCCCACACTCCTCAAAAAAGGCCAACAAAAAACAG AGGGCAGACTGGAGTCTGTTCTGTGTGTTTTCCTGGAGCCTGTGCCTATGTCAC--TG CAATTITCAGGAGACATATTCAACTCCTCTGCTCTTCCAAACCTGGTGTCTATCCGGCAG -GTCTCCCTGACCTGCTCTATGCCCCACACCCTAC--GTGCCGTGGCTCTGTGCAG TGT--ACGIAGATAGCTCTCG-CCTGGGTCTGTGCTGTTTGTCGTGAAAAGCTTAA--TG -AGACTCCCACTCTGCACACACTCCCACCTCTCAAGCCTCCAACCTCTTGGCCAGA TTGGGCTCATTAAT-GTCGTTGCCTGCCCATCTG-CATGAATGACAGGCAGCTCCCCATG TTGCGCTCATTAATGGTCGTTGCCTGCCCATCTGCCATGAATACCAGCTCCCCATG GTGGTCTGCCT-GTGAGCTCTTCAAGTTCTTAATCCTTAACTCCAGGATTAGCTCCCAAGT GCGCTGAGACCCAGCCA - - - GCACACTTCTGGCCCTTCTCCCTGCCTCAATCTAAAAGCA GTGCCACACCCTCCAAA-GTGGAATAGAAAGAAGTTCATGAGTAAG-GGCTGCAAGGAAT TCTTATCCTGGCCA-----CATGTCCTCCGTGCACA----CACCCAATGGAGTTA AACTTCAAGTCGGAGGTCATGGTACCAGTTAAAGCCAGTGGCA-GCTCCCACTGCCGGGC DP OY DP oy da Oy Oy Oy δy QQ Qy Db oy Db Dp φ g ΟŸ qq q òγ Dp Óγ Ωÿ δ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention discloses a novel polypeptide-human CaM kinase I 39.05, polynucleotide for coding the polypeptide and method for producing this polypeptide by DNA recombination technology. The polypeptide is useful for treating diseases such as nervous disease, arrhythmia, tumour and growth development disturbance disease. The present sequence represents the human CaM kinase I 39.05 polypeptide encoding cDNA.
----AGTTTCCTCGCCCTCCACCCTCCAGCTTCATGCTCAGTGTTGTGCTTAATAAAA 2419
          2606 TATGTCCTCGGCCCGTCGCACCCGTCCAGGCTTCATGCTCAGAGTTGTGCTTAATAAAA 2665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGAAGCAAAGACTGACTGGGAAGCTCTTTGCTCTGAAGTGCATC---AAGAAGTCACC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 AGCTGAAGAGAAGCAACTGGCAAGCTCTTTGCTGTGAAGTGTATACCCTAAGAAGGGGCT 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polypeptide human CaM kinase I 39.05 and polynucleotide for encoding said polypeptide -
                                                                                                                                                                                          CaM kinase I 39.05; nervous disease; arrhythmia; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 24; Length 1565;
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Pred. No. 4.3e-132;
0; Mismatches 274; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1565 BP; 408 A; 394 C; 410 G; 353 T; 0 other;
                                                                                                                                                                                                                                                              /*tag= a
/product= "human CaM kinase I 39.05"
                                                                                                                                                                    Human CaM kinase I 39.05 polypeptide encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 26-27 (disclosure); 35pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                          (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
                                                                                                                                                                                                                                          Location/Qualifiers
18..1085
                                                 TGGACATATTTTCTCTAAAAAA 2443
                                                                                                            BP.
                                                                                                           ABL60905 standard; cDNA; 1565
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                                                                                                                                                                                                                                                                                                                                    07-JUL-2000; 2000CN-0119405
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                                                                                                                                                  (first entry)
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P-PSDB; ABB08178.
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                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                  23-SEP-2002
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                                                                                                                              ABL60905;
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                                                                                                                                                                                           Human;
2365
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ABL60905
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Human kinase; PKIN; gene therapy; adenocarcinoma; immune disorder; gout; cancer; allergy; sarcoma; leukaemia; acquired immune deficiency syndrome; AIDS; Addison's disease; microbial infection; inflammation; osteoporosis; atherosclerosis; cardiovascular disease; myocardial inferction; anaemia; myasthenia gravis; cirrhosis; cataract; growth and development disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            960 GAACTTTGCTAAGAGCAAGTGGAGGCAAGCCTTCAACGCAGCAGCTGTGGTGCACCACCAT 1019
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302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            914 AAACTTTGCCAAGAGCAAATGGAGACAGCATTTAATGCCACGGCCGTCGTGAGATTT
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                   GCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCTGGAGCGGGGTGTCTACACACAGAGAA
                                                                                                                                                                                                                                                GGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGCCAGTGAAATACCTACATGAAATGG
                                                                                                                                                                                                                                                                      CATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCTTTACCTTACCCTGAAGAGAACTC
                                                                                                                                                                                                                                                                                                                                                     543 TAAGATCATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGG----CATCATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                CACTGCCTGTGGGACCCCCAGGCTACGTGCTCCAGAAGTGCTGGCCCAGAAACCCTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAGGCTGTGGATTGCTGGTCCATCGGCGTCATCACCTACATATTGCTCTGTGGATACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       614 CAAAGCCGTTGACTGCTGGTCCATCGGAGTGATTGCCTACATCTTGCTCTGCGGCTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCGTTCTATGAAGAAACGGAGTCTAAGCTTTTCGAGAAGATCAAGGAGGGCTACTATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human kinase (PKIN)-11 cDNA.
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cids encoding them. PRIN is used as vaccine and in gene therapy. PRIN is used in the prevention, diagnosis and treatment of diseases cancers, adenorarized line, leavention, diagnosis and treatment of diseases cancers, adenorarized line prevention, diagnosis and treatment of diseases cancers, adenorarized line prevention, surcoma, immune disorder, Addison's disease, acquired immune deficiency syndrome (AIDS), anaemia, asthma, allergies, gout, microbial infections, cardiovascular disease and/or inflammation, myasthenia gravia, atheroselerosis, cirrhosis, osteoproresis, mycoardial infarction, cataract, disease, lipid disorder, seizure disorder, pulmonary embolism, daucher's disease, ilpid disorder, ipid storage disease, pick's disease, Tay-Sachs disease, renal disease and obesity.

FRIN may be used to treat disorders associated with decreased PRIN expression by rectifying mutations or deletions in a patient's genome that affect the activity of PRIN by expressing inactive proteins or to supplement the patients own production of PRIN. PRIN nucleic acids into used to produce the PRIN polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. PRIN nucleic acids and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar control and control of prince the presence of similar may need of restorative therapy. The present sequence is human PRIN-II
seizure disorder; pulmonary embolism; Gaucher's disease; lipid disorder; lipid storage disease; Pick's disease; Tay-Sachs disease; renal disease; obesity; restorative therapy; immunomodulatory; vaccine; cardiovascular; antimicrobial; cytostatic; antiinflammatory; asthma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yao MG;
SA, Lu Y;
Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acids, useful for preventing diagnosing and inflammation and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to human kinases (PKIN) and the nucleic acids encoding them. PKIN is used as vaccine and in gene therapy. PKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l AR, Tribouley CM, Kearney L, Griffin JA, Nguye a DAM, Lal P, Burford N, Khan FA, Walia NK, Yao Burrill JD, Marcus GA, Zingler KA, Recipon SA, Phornton M, Tang YT, Hafalla A, Elliott VS, Baug nkumar J, Borowsky ML, Au-young J, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 20.6%; Score 504.6; DB 22; Length 1661; Local Similarity 71.3%; Pred. No. 4.4e-132; nes 695; Conservative 0; Mismatches 274; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1661 BP; 408 A; 452 C; 448 G; 353 T; 0 other;
                                                                                                                                                                                                /*tag= a
/product= "Human PKIN-11 protein"
                                                                                                                                                Location/Qualifiers
159..1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 159; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     2000US-199021P.
2000US-200226P.
2000US-202339P.
2000US-203505P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-2000; 2000US-207739P. 01-JUN-2000; 2000US-208795P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                              20-APR-2001; 2001WO-US12992
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Bandman O, Lu DAM, Lal
Patterson C, Burrill JD,
Policky JL, Thornton M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Policky JL, Thornton M,
Walsh RT, Ramkumar J,
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P-PSDB; AAE11777.
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05-MAY-2000;
11-MAY-2000;
18-MAY-2000;
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                                                                                                            sapiens
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GAACTTTGCTAAGAGCAAGTGGAGGCAAGCCTTCAACGCAGCAGCTGTGGTGCACACAT 1019
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            GGTGAAGCAAAGACTGACTGGGAAGCTCTTTGCTCTGAAGTGCATC---AAGAAGTCACC
                                                                                  TGCCTTCCGGGACAGCAGCCTGGAGATGAGATTGCTGTGTTGAAAAAGATCAAGCATGA
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Best_Loca Matches 99

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2000US-0552317.
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2000US-0620312.
2000US-0653450.
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leukaemia; ss.
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a kinase polypeptide. The kinase polynucleotides and polypeptides are useful in therapeutic, diagnostic and pharmacogenic applications. They are useful for the detection of mutant kinases, or inappropriately expressed kinases for the diagnosis of a disease or disorder. They are useful for screening for drugs (or high throughput screening of combinatorial libraries) effective in the treatment of symptomatic or phenotypic manifestations of that disease or disorder. The polynucleotide sequence is useful as a source of probes and primers, which can be used to screen libraries, isolate
                                                                                                                                                                                                                                                                             Novel isolated human kinase polynucleotide that shares structural similarity with animal kinases including calcium/calmodulin-dependent protein kinases and serine/threonine protein kinases, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 504.6; DB 22; Length 1671;
Pred. No. 4.4e-132;
0; Mismatches 274; Indels 6;
                                                                                                                                                                                                                     B,
                                                                                                                                                                                                                      Zambrowicz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1671 BP; 453 A; 437 C; 448 G; 333 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clones, and prepare cloning and sequencing templates
                       Nucleotide sequence of a human kinase polypeptide
                                                                                                                                                                                                                     Friedrich G,
                                               human disease; human disorder; ss
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                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 32; 32pp; English.
                                                                                                                                                                                                                      Turner
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71.3%;
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                                                                                                                                                                                                                    Scoville J,
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es 695; Conserv
                                               Human; kinase;
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                                                                                                                                                                      07-DEC-1999;
                                                                                                                                                                                                                                                                                                                   therapeutics
                                                                        Homo sapiens
 22-AUG-2001
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Syy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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779

PPR X PPR X

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Human kinase; PKIN; gene therapy; adenocarcinoma; immune disorder; gout; cancer; allergy; sarcoma; leukaemia; acquired immune deficiency syndrome; AIDS; Addison's disease; microbial infection; inflammation; osteoporosis; atherosclerosis; cardiovascular disease; myocardial infarction; anaemia; myasthenia gravis; cirrhosis; cataract; growth and development disorder; seizure disorder; pulmonary embolism; Gaucher's disease; lipid disorder; lipid storage disease; plick's disease; pray-Sachs disease; renal disease; asthma; obesity; restorative therapy; cytostatic; immunomodulatory; antimicrobial; cardiovascular; antilnflammatory; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                     1051 cecregreacaccecercaacaaaacarceacgagreegreegeceagareegaa 1110
                      720 CCCGTTCTATGAAGAAACGGAGTCTAAGCTTTTCGAGAAGATCAAGGAGGCTACTATGA
                                                                                                                                                                                                                                                                                                             GAACTITGCTAAGAGCAAGTGGAGGCAAGCCTTCAACGCAGCAGCTGTGGTGCACCACAT
   543 TAAGATCATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGG----CATCATGTC
                                                                       CACTGCCTGTGGGACCCCAGGCTACGTGGCTCCAGAAGTGCTGGCCCAGAAACCCTACAG
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279..12129
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/product= "Mature human PKIN-2 protein"
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159..278
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                                                                                                                                                                                                                                                                                                                      The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, heamostatic and thrombolytic activity, chemotactic/chemokinetic activity, heamostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed
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                                                                                                           Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 20.6%; Score 504.6; DB 22; Length 1733; Best Local Similarity 71.3%; Pred. No. 4.5e-132; Matches 695; Conservative 0; Mismatches 274; Indels 6;
                                                                                                          Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1733 BP; 439 A; 467 C; 462 G; 365 T; 0 other;
                                                                                                          Ma Y,
Xue AJ,
                                                                                                                                                                                                                                     nsefnl
                                                                                                        Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 841; 10078pp; English.
                                                                                                                                                                                                                                 Novel nucleic acids and polypeptides, us such as central nervous system injuries
14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                2001-442253/47.
                                                                       (HYSE-) HYSEQ INC
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C.N.S disorders.
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                                                                                                        YT,
                                                                                                          Tang
Wang
Zhao
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                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to human kinases (PKIN) and the nucleic acids encoding them. PKIN is used as vaccine and in gene therapy. PKIN is used in the prevention, diagnosis and treatment of diseases cancers, adenocarcinoma, leukemia, sarcoma, immune disorder, Addison's disease, adenocarcinoma, leukemia, sarcoma, immune disorder, Addison's disease, acquired immune deficiency syndrome (AIDS), anaemia, athma, allergies, gout, microbial infections, cardiovascular disease and/or inflammation, myasthenia gravis, atherosclerosis, cirrhosis, osteoporosis, myocardial infaction, cataract, growth and development disorder, lipid storage infarction, cataract, growth and development disorder, seizure disorder, glassase, Pkick's disease, renal disoraer, seizure disorder, pkin may be used to treat disorders associated with decreased pkin.

Cexpression by rectifying mutations or deletions in a patient's genome that affect the activity of PKIN by expressing inactive proteins or to supplement the patients own production of PKIN, PKIN nucleic asset to produce the PKIN polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. PKIN nucleic acid and its complementary sequences may also be used as DNA probes in nucleic acid sequences in samples and therefore which patients may be nucleic acid sequences in samples and therefore which patients may be need of restorative therapy. The present sequence is human PKIN-2 cDNA.
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                                                                                                                                                                                                      SA, Lu Y;
Baughn MR;
                                                                                                                                                                             Nguyen DB;
Yao MG;
                                                                                                                                                                                                                                                                                                                    Human kinases and nucleic acids, useful for preventing diagnosing and treating cancers, inflammation and immune disorders -
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                                                                                                                                                                       Yue H, Gandhi AR, Tribouley CM, Kearney L, Griffin JA, Nguye
Bandman O, Lu DAM, Lal P, Burford N, Khan FA, Walia NK, Yac
Patterson C, Burrill JD, Marcus GA, Zingler KA, Recipon SA,
Policky JL, Thornton M, Tang YT, Hafalia A, Elliott VS, Bauu
Walsh RT, Ramkumar J, Borowsky ML, Au-young J, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 503; DB 22; Length 1736;
Pred. No. 1.3e-131;
0; Mismatches 275; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1736 BP; 463 A; 456 C; 466 G; 351 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 151-152; 166pp; English
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                                        2000US-200226P.
2000US-202339P.
2000US-203505P.
2000US-205564P.
                                                                    11-MAY-2000; 2000US-203505P.
18-MAY-2000; 2000US-205564P.
26-MAY-2000; 2000US-207739P.
01-JUN-2000; 2000US-208795P.
20-APR-2001; 2001WO-US12992
                                                                                                                                             (INCY-) INCYTE GENOMICS INC
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Matches 694; Conservative
                                                                                                                                                                                                                 JL, TRULL...
TRamkumar J,
                                                                                                                                                                                                                                                                         WPI; 2001-611740/70.
P-PSDB; AAE11768.
                                        28-APR-2000;
05-MAY-2000;
                            20-APR-2000;
                                                                                                                                                                                                                                                 Gururajan R;
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Human, nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                      GGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAATACCTACATGAGAATGG
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GCTGGTGTCCCGGTGGAGAGCTGTTTGACCGGATAGTGGAGAAGGGGGTTTTATACAGAAA
                                                                                                                  543 TAAGATCATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGG.---CATCATGTC
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metabolic disorder; immune related disease; neurological disorder; neurodegenerative disorder; inflammatory disorder; infectious disease; reproductive disorder; gene therapy; ss.
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                                                  CATCGTCCACAGAGACTTAAAGCCCCGAAAACCTGCTTTACCTTACCCTGAAGAGAACTC
                                                                                                                 TAAGATCATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGG----CATCATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein kinase; PTK; STK; cancer; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Martinez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotide sequence encoding human protein kinase #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Manning G,
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Flanagan P,
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                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM4213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and chromotars.
                                                                                                                                                                                                                    Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               422
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                                                                                                                                                                                                                                                                                                                                     for treating disorders
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                                                                                                                                                                                                                    Ren F, W
Zhang J;
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                                                                                                                                                                                                                    Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2164 BP; 557 A; 542 C; 560 G; 505 T; 0 other;
                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                              Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 4413; 10078pp; English
                                                                               2000US-0620312.
2000US-0653450.
2000US-0662191.
                                              2000US-0552317.
2000WO-US34263
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2000US-0727344
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                                                                                                                                                                                 (HYSE-) HYSEQ INC
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                                                                              19-JUL-2000; 2
03-AUG-2000; 2
14-SEP-2000; 2
                             21-JAN-2000;
25-APR-2000;
09-JUL-2000;
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29-NOV-2000;
26-DEC-2000;
                                                                                                                                                                                                              Tang YT,
Wang J, W
Zhao QA,
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                                                                                                                                     AASO6701-AASO6757 encode for novel human protein kinases #1-57. The novel protein kinases have been identified as members of the tyrosine or serine/threonine kinase (PTK and STK) families. The polynucleotides encoding protein kinases and the polypeptides may be used in the prevention, diagnosis and treatment of diseases associated with imappropriate kinase expression. For example, they may be used to treat cancers (especially cancers of hematopoletic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), immune related diseases (e.g. rheumatoid arthritis), neurological disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. parkinson's disease), inflammatory disorders (e.g. infertility). Additionally, polynucleotides encoding protein kinases may be used as of antibodies against the protein kinases and in assays. The protein kinase polypeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify modulators of protein kinase expression and activity.
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                                                preventing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 AAAACCTTCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTTTTCCTGGTG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding human kinase polypeptides, useful for preven diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 AAGCAAAGACTGGGAAGCTCTTTGCTCTGAAGTGCATC---AAGAAGTCACCTGCC
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1074 BP; 313 A; 258 C; 276 G; 227 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 502.2; DB 22;
Pred. No. 1.7e-131;
0; Mismatches 273;
                                                                                                            Example 1; Figure 1; 433pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 20.5%;
al Similarity 71.3%;
692; Conservative (
2001-343950/36
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              P-PSDB; AAU03508
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Matches
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TTTGCTAAGAGCAAGTGGAGGCAAGCCTTCAACGCAGCAGCTGTGGTGCTGCACCACATGAGG 1023
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                                                                                                                                                                   843
                                                                                                         GCTGTGGATTGCTGGTCCATCGGCGTCATCACCTACATATTGCTCTGTGGATACCCCCCG
                        TICTATGAAGAAACGGAGTCTAAGCTTTTCGAGAAGATCAAGGAGGGCTACTATGAGTTT
                                                                                                                                                                   GAGTCTCCATTCTGGGATGACATTTCTGAGTCAGCCAAGGACTTTATTTGCCACTTGCTT
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/transl_except= "(pos: 838..843, aa: Ala)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of a human kinase polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; kinase; human disease; human disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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Sands AT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1024 AAGCTACACAT 1034
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P-PSDB; AAB84360.
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The present sequence encodes a kinase polypeptide. The kinase polynucleotides and polypeptides are useful in therapeutic, diagnostic and pharmacogenic applications. They are useful for the detection of mutant kinases, or inappropriately expressed kinases for the diagnosis of a disease or disorder. They are useful for screening for drugs (or high throughput screening of combinatorial libraries) effective in the treatment of symptomatic or phenotypic manifestations of that disease or disorder. The polynucleotide sequence is useful as a source of probes and primers, which can be used to screen libraries, isolate clones, and prepare cloning and sequencing templates.
                                                                                        TTTGCTAAGAGCAAGTGGAGGCAAGCCTTCAACGCAGCAGCTGTGGTGCACCACATGAGG 1023
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                                                                                                                                                                    ATTGTGACCCTGGAGGACATCTATGAGAGCACCACCACTACTACTGGTCATGCAGCTT 366
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                                  AAAACCTICATITITATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTTTTCCTGGTG 189
                                                       AAGATCTTCGAGTTCAAAGAGACCCTCGGAACCGGGGCCTTTTCCGAAGTGGTTTTAGCT 120
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Human; death domain-containing receptor; DDCR; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmological; gene therapy; immunodeficiency disease; Acquired immune deficiency syndrome; AIDS; leukaemia; autoimmune disease; systemic lupus erythematosus; hyperproliferative disorder; neoplasm; cerebrovascular disorder; cerebral ischaemia; angiogenesis; cardiovascular disorder; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; neurodegenerative disease; Alzheimer's disease; parkinson's disease; ocular disorder; corneal infection; degenerative disease; SWA, apoptosis; spinal muscular atrophy; epithelial cell proliferation; infection; cancer; wound healing; skin aging; chemotaxis; HDPVZ91 clone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNAs and their corresponding proteins. DDCR CDNA and protein are used to prevent, treat or ameliorate a medical condition in mammals. They are also used in diagnosing a pathological condition in mammals. Susceptibility to a pathological condition. The DDCR protein and its antibodies are used in the diagnosis and treatment of disorders such as immunodeficiency diseases (e.g. Acquired immune distance deficiency syndrome (AIDS), leukaemia) autoimmune diseases (e.g. systemic lupus crythematosus, rheumatoid arthritis), hyperproliferative disorders (e.g. cardiac arrest), neurodegenerative diseases (e.g. Alzheimer's (e.g. cardiac arrest), neurodegenerative diseases (e.g. Alzheimer's infection), degenerative disorders of the plasorders diseases, parkinson's disease), coular disorders (e.g. cardiac arrest), neurodegenerative diseases (e.g. Alzheimer's infection), degenerative disorders of the placenta or uterus and clusters are used by bacteria, viruses and fungi. The DDCR proteins are used to aid wound healing and epithelial cell proliferation, remandant since in culture of primary fissues, to remark and in chancaevier of primary fissues, to
                                                         domain-containing receptor (DDCR) cDNA from HDPV291 clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New death-domain containing receptor polynucleotides and polypeptides useful for treating and diagnosing cancer \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Human death domain-containing receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The patent discloses novel death domain-containing receptor (DDCR)
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R) cDNA from clone HDPV291 (ATCC No: PTA839).
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24-NOV-1999;
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The present sequence is the coding sequence for Murine Dendritic Cell Kinase 3 (MDCK-3). The protein encoded by the present sequence is useful for treating a variety of disorders listed in the disclosure of the specification, including autolimmune disorders, allergic reactions, myeloid or lymphoid cell deficiencies, wound healing and tissue repair and replacement, burns, inclsions and ulcres, periodontal disease, inflammatory diseases, tumours and bacterial, viral or fungal infection. MDCK-3 is a member of the Ca2+/calmodulin-dependent kinase family.
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                                                                     Murine; Dendritic Cell Kinase; MDCK-3; autoimmune disorder wound healing; periodontal disease; inflammatory disease; infection; Ca2+/calmodulin-dependent kinase family; ss.
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Pred. No. 1.1e-128;
0; Mismatches 279;
                                        Dendritic Cell Kinase 3 coding sequence
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                                                                                                                              TITGAGICICCATICIGGGAIGACATITCIGAGICAGCCAAGGACTITATITGCCACTIG 840
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                         ACTGCCTGTGGGACCCCCAGGCTACGTGCTCCAGAAGTGCTGGCCCAGAAACCCTACAGC 660
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600 GATGCCAGCACTCTCATCCGCCAGGTCCTGGATGCCGTATACTATCTCCACAGAATGGGC 659
                                                                                            544 AAGATCATGATCACTGACTTTGGTCTGTCCAAGATGGAACAGAATGG---CATCATGTCC
               484 ATCGTCCACAGAGACTTAAAGCCCGAAAACCTGCTTTACCTTACCCCTGAAGAGAACTCT
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Search completed: March 14, 2003, 14:17:14 Job time: 574 secs

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  (without alignments)
  10211.378 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                         OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		ID		BM547443	BI084897	BI084101	BI821474	BI824483	BI818261
		DB	1	13	13	13	13	13	13
		Query ore Match Length DB I		1126	996	1048	808	740	742
	dР	Query Match	1 1 1 1 1	39.4	33.8	32.8	32.5	30.1	29.5
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BM921532 B1772626 BM807335 BG715920 B1753035 BQ934044 BG293660	B1667965 B1834635 BQ086330 AL134342 BQ102407	AL560091 AW016039 AW251224 BM944418 AA838372 AL556476 BQ949629 BG168668	AW254051 BI758466 AW52224 BE562540 BM919261 AW826802 AW520558 BG702279 BI545845 AL578723	BG895406 B0066920 B161267 B1761267 B266955 BM728430 BM728430 BF143967 ALIGNMENT	1126 b MGC_125 3 ordata;	1.nih.gov/ f Health, sberg, Ph. nih.gov nvitrogen tion: Life by: The I gencourt B WGC clone A.G.E. Cc
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us-09-960-643-1.rst

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Site_1: Ecory (destroyed); Site_2: Not!; RNA source pool of three ovaries, from females ranging in age from 38 to of three ovaries, from females ranging in age from 38 to of three states, from females ranging in age from 38 to so three ovaries, from females ranging in age from 38 to of three states destroyed upon cloning). Average insert size 1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Glone (invitrogen). Research Genetics tracking code 036. "Total converse of the converse 
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Site_2: EcoRI: cDNA made by oligo-dT priming.
Directionally cloned into EcoRY/XhoI sites using the
following 5' adaptor: GGCAGCAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIO84897 966 bp mRNA linear EST 20-JUN-2001 602869466T1 NIH_MGC_102 Homo sapiens CDNA clone IMAGE:5013856 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 966)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: agabbar Temail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM1820 row: d column: 17
High quality sequence stop: 832.
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                      GATTGACGGAAACACGCCCC--TCCACCGGGACATCTACCCATCAGTCAGCCTCCAGATC
                                                                                      CTTGAGAAGGATCCGAACGAGCGGTACACCTGT--GAGAAGGCCTTGAGTCATCCC--TG
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No. 2.1e-209;

    966
    /organism="Homo sapiens"
/db_xref="taxon:9606"

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BI084897
BI084897.1 GI:14503227
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/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Corgan: salivary gland: Vector: poTB7; Site_1: XhoI;
Site_2: ECORI; CDNA made by oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the
Directionally cloned into ECORI/XhoI sites using the
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-CDNA
synthesis Kit (Stratagene) and Supersoript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1048e); NIH-MCC http://mgc.nci.nih.gov/. NIH-MCC http://mgc.nci.nih.gov/.
                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Arror
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM1820 row: d column: 17
High quality sequence stop: 853.
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Pred. No. 8.1e-203;
0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:5013856"
/clone_lib="NIH_MGC_102"
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 GI:14502431
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Best Local Similarity 93.1%;
Matches 885; Conservative
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pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bp mRNA linear EST 04-OCT-2001
sapiens cDNA clone IMAGE:5179336 5',
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NIH-WGC http://mgc.nci.nih.gov/.
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2025 GACAGGCAGCTCCCCATGGTGGTGTGTGAGCTCTTCAAGTTCTAATCGTTAACTCC
                                                                                                                                                                                  2085 AGGATTAGCTCCCAAGTGCGCTGAGACCCAGCCAGCACACTTCTGGCCCTTCTCCCTGCC
                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-remail.nih.gov
Tissue procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11447 row: c column: 17
                                           2203 -GGGCTGCAAGGAATTCTTATCCTGGCCACATGTCCTCCGTGCACACCCCAATGGAGTT
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/db_xref="taxon:9606"
/clone="IMAGE:5179336"
/clone_lib="NHH_MGC_115"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 808.
Location/Qualifiers
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603038366F1 NIH_MGC_115
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BI821474
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male lung, age 27; and 1 male testis, age 69. Library 1: oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, Library is normalized and enriched for full-length clones and was constructed by Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
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es 796; Conserv
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//note="Organ: pooled brain, lung, testis; Vector:
pcMv-SPORT6; Site_1: Not1; Site_2: EccRv (destroyed); RNA
source anonymous pool of 6 male brains, age 69. Library is
oligo-dT primed and directionally cloned (EccRv site is
destroyed upon cloning). Average insert size 18 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C
Gruber (Invitrogen). Research Genetics tracking code
oligi. Note: this is a NHL MC Library."

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BI824483 740 bp mRNA linear EST 04-OCT-2001 603038855F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5179957 5',
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 740)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1448 row: m column: 14
High quality sequence stop: 709.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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603032510F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173587 5', BISH2261
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fordy-SpoRT6; Site_1: Not!; Site_2: BEORV (destroyed): RNA
source anonymous pool of 6 male brains, age range 23-27; I
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (Eroxv site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length chones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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NIH-MGC http://mgc.noi.nih.gov/.
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/clone_lib="NIH_MGC_115"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1068)
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                                                                                              GCAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCCTGGAGCGGGGTGTCTACACAGA 419
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                                                                                                                                                                                   ACCTGCCTTCCGGGACAGCAGCCTGGAGAATGAGATTGCTGTGTTGAAAAAGATCAAGCA
                                       1;
                       Length 742;
                                       Indels
                       DB 13;
                       Score 720.8; DB 13
Pred. No. 2.4e-181;
                                      0; Mismatches
168
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197
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BM921532.1 GI:19371911
                      29.5%;
99.6%;
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Contact: Nobel: Strausbry, Fil.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM1278B row. b column: 19
High quality sequence stop: 592.
Location/Oualifiers
I. 1068

| John Exter="Texaco:9606" |
| Clone="Texaco:9606" |
| Clone=
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                                                                                                                 Contact: Robert Strausberg, Ph.D.
NIH-MGC http://mgc.nci.nih.gov/
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BM807335 1129 bp mRNA linear EST 05-MAR-2002
AGENCOURT_6575096 NIH_MGC_124 Homo sapiens CDNA clone IMAGE:5732298
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1129)
                                                                                                                                                          189 TTCCTGGTGAAGCAAAGACTGACTGGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCA 248
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                     AACATCCGGAAAACCTTCATTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTT 188
                                                                                                                                                                                                             GAAAACATTGTGACCCTGGAGGACATCTATGAGAGCACCACCACCTACTACCTGGTCATG 360
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BM807335
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                                                                                                                                                                                                                                                                                                                                BI772626 812 bp mRNA linear EST 25-SEP-2001
603060879F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5210299 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: capbbs-Temail.nih.gov
Email: capbbs-Temail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genemics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1527 row: m column: 20
High quality sequence start: 2
High quality sequence start: 2
High quality sequence stop: 808.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) (Uppublished (1999)
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614 ACCTGCCTGTGGGACCCCAGGCTACGTGGCTCCAGAAGTGCTGGCCCAGAAACCCTACAG
                                                                     A-CTGCCTGTGGGACCCCAGGCTACGTGGCTCCAGAAGTGCTGGCCCAGAAACCCTACAG
                                                                                                                                        CAAGGCTGTGGATTGCTGGTCCATCGGCGTCATCACCTACATATTGCTCTGTGGATACCC
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Pred. No. 2.7e-179;
                                                                                                                                                                                                           720 CCCG-TICTAIGAAGAAACGGAGICIAAGCITII 752
                                                                                                                                                                                                                              CCCCCTCCTATGAAGAAACGGAATCTAACCTTTT 767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5210299"
/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
BI772626
BI772626.1 GI:15764204
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Best Local Similarity 91.0%;
Matches 801; Conservative
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KEYWORDS
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BI772626
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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G. E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM10688 row: e column: 17
High quality sequence stop: 766.
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                                                                                                                                                                 1 (bases 1 to 824)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
661 AAGGC----TGTGGATTGCTGGTCCATCGCCGTCATCA-CCTACATATTGCTCTGTGGATA
                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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    824
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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BG715920
BG715920.1 GI:13995107
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BG715920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                             cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 AACATCCGGAAAACCTTCATTTTTATGGAAGTGCTGGGATCAGGAGCTTTCTCAGAAGTT 215
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                                                                                                                                                                                                                                                                                           1. .1129
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5732298"
/clone_lib="NIH_MGC_124"
                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="hippocampus"
/lab_host="DH108"
                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
                                                                                                                                                                                                                             High quality sequence start: 11
High quality sequence stop: 651.
Location/Qualifiers
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Matches 800; Conserv
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                                                                      CTGGAGGCAATGGGTCGAAAGGAAGAAGATGACTGCAGTTCCTGGAAGAAAAAGAACAGACCACC 120
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 731)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                    9
                                                     97
                                           181 TTCCTGGTGAAGCAAAGACTGACTGGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCA
                                                                              TGGAGTGGGAGCTCAAGCAGGATTCTTCCCGAGTCCCTGGCATCCTCAGAAGCTTCAACT
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Pred. No. 4e-176;
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Contact: Robert Strausberg, Ph.D.
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               0;
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      96.98;
       Local Similarity 96.9
nes 747; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BI753035
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/u...()
// Crganism="Homo sapiens"
// Ab_xref="taxon:9606"
// Clone="INAGE:1519632"
// Clone="INAGE:1519632"
// Clone="INAGE:114"
// Iab_host="DHIOB"
// Iab_host="DHIOB"
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// Iab_host="Cornor of the cornor of
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The T.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIL491 row: g column: 12
High quality sequence stop: 729.
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Pred. No. 1.6e-175;
0; Mismatches 0;
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Best Local Similarity 99.7%;
Matches 721; Conservative
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DEFINITION
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BO934044
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 905)
NIH-WG http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:1000"
/db_xref="taxon:1000"
/clone_lb="lb="NHA" MGC_130"
/lab_host="DH10B (Ghage-resistant)"
/note="Organ: otocysts; Vector: pCMV-SPORT6.1.ccdb;
Site=1: Booky, Site_2: Nott; Cloned unidirectionally.
Primer: Oilgo dT. Average insert size 1.95 kb.
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68 GAGCCCTGGCTTCTCAGGCAGCTTCAACTCTGGAGGACATGGGGGCGTAAGGAGGAGGAG 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 653.6; DB 14; Length 905;
Pred. No. 2.5e-163;
0; Mismatches 79; Indels 4;
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217 c 240
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llarity 90.0%;
Conservative
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es 745;
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ORIGIN
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                                                                                                                                    RESULT 12
BQ934044
LOCUS
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AUTHORS
TITLE
JOURNAL
COMMENT
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BG293660 818 bp mRNA linear EST 21-FEB-2001 602390529F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4502479 5',
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 818)
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.i column: 08
High quality sequence stop: 765.

I. .818
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Contact: Roberts Treasperation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
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AACCTGCTTTACCTTACCCCTGAAGAGAACTCTAAGATCATGATCACTGACTTTGGTCTG
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BG293660
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pBluescript KS+); Site_1: BamHI; Site_2: SalI-TXDI (gtcgag plucer); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2: SalI-TXDI (gtcgag insert size-selected for average insert size 2: Sk band for full-length clones and constructed using the constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

a 156 c 177 g 146 t
5 bp mRNA linear EST 12-SEP-2001 sapiens cDNA clone IMAGE:5312346 5',
                                                                                                             Homosapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 656)
S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
L Onpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Constitution and Piero Carninci (RIKEN)
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Inoyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
High quality sequence stop: 643.
                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 TTTCCTGGTGAAGCAAAGACTGACTGGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTC
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Pred. No. 5e-137;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="hypothalamus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5312346"
/clone_lib="NIH_MGC_96"
               603292877F1 NIH_MGC_96 Homo
                                   mRNA sequence.
BI667965
BI667965.1 GI:15582198
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ilarity 97.6%;
Conservative
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                                                                                                                                                                                                                                                                                                        31 GAGTCCCTGGCATCCTCAGAAGCTTCAACTCTGGAGGCAATGGGTCGAAAGGAAGAAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGTCTGCGGTGAAATACCTTCATGAGAATGGCATCGTCCACAGAGATCTAAAAGCCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGATCCTGGAGCGGGGTGTCTACACAGAAGGATGCCAGTCTGGTGATCCAGCAGGTC
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                                                                                                                                                                                                                                   Score 590.6; DB 12;
Pred. No. 1.7e-146;
0; Mismatches 89;
                                                                                                                                                                                                                                     24.1%;
88.0%;
                                                                                                                                                                                                                                                                       677; Conservative
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pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dr primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 0.05: Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                               BI834635 554 bp mRNA linear EST 04-OCT-2001 603090418F1 NIH_MGC_120 Homo saplens cDNA clone IMAGE:5229245 5',
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                             GAGAAGGATGCCAGTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAATACCTACATGAG 477
                                                                                   1 (bases 1 to 554)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs.remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Library Sequence stop: 554.
High quality sequence stop: 554.
GCAGCTTGTTTCTGGTGGGGAGCTCTTTGACCGGATCC--TGGAGCGGGGTGTCTACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.3%; Score 522; DB 13; Length 554; 96.0%; Pred. No. 3.1e-128; Live 0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 554
/organism="Homo sapiens"
/db_xxef="taxon:9606"
/clone="IMAGE:5229245"
/clone=lib="NIH_MGC_120"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                 TGTCCACTGCCTGTGGGACCC 616
                                                                                                                                                                                                                                                                                                                                                                                                                                              BI834635.1 GI:15946185
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                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
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                                                                                                       262 CTGGAGAATGAGATTGCTGTTGAAAAAGATCAAGCATGAAAACATTGTGACCCTGGAG
                                                                                                                                                                                                   322 GACATCTATGAGAGCACCACCACTACTACTGGTCATGCAGCT-----TGTTT
                                                                                                                                                                                                                 CTGGTGGGGAGCTCTTTGACCGGATCCTGGAGCGGGGTGTCTACACAGAGAAGGATGCCA
                                                                                                                                                                                                                                                                                                           GTCTGGTGATCCAGCAGGTCTTGTCGGCAGTGAAATACCTACATGAGAATGGCATCGTCC
                                                                                                                                                                                                                                                                                                                       491 ACAGAGACTTAAAGCCCGAAAACCTGCTTTACCTTACCCCTGAAGAGAACTCTAAGATCA
                                                                                                                                                                                                                                                                                                                                                                       <u> ACTGGGAAGCTCTTTGCTCTGAAGTGCATCAAGAAGTCACCTGCCTTCCGGGACAGCAGC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: March 14, 2003, 15:22:05 Job time : 3891 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGACCCCAGGCTAC 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGACCCCAGGCTAC 554
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